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(54) Title: NOVEL MOLECULES OF THE TNFR-LIGAND-RELATED PROTEIN FAMILY AND USES THEREOF			
(57) Abstract			
<p>Novel TANGO-69 nucleic acid molecules and polypeptides are disclosed. In addition, the invention provides isolated TANGO-69 fusion proteins, antigenic peptides and anti-TANGO-69 antibodies. The invention also provides TANGO-69 recombinant expression vectors containing nucleic acid molecules of the invention, host cells into which the expression vectors have been introduced and non-human transgenic animals in which a TANGO-69 gene has been introduced or disrupted. Diagnostic, screening and therapeutic methods utilizing compositions of the invention are also provided.</p>			
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NOVEL MOLECULES OF THE TNFR-LIGAND-RELATED
PROTEIN FAMILY AND USES THEREOF

Background of the Invention

Members of the tumor necrosis factor receptor
5 (TNFR) superfamily regulate a diverse range of cellular
processes including cell proliferation, programmed cell
death and immune responses. Characteristically, these
receptors are transmembrane (type 1) glycoproteins having
cysteine-rich subdomains in their extracellular, ligand
10 binding domain (Gruss (1996) *Int. J. Clin. Lab. Res.*
26:143-159).

A recently identified member of the TNFR
superfamily is the herpesvirus entry mediator (HVEM)
(Montgomery et al. (1996) *Cell* 87:427-436). HVEM
15 mediates the entry of many strains of herpes simplex
virus (HSV) into cells. Studies have revealed that HSV
initiates infection by binding cell surface
glycosaminoglycans. To actually enter the cell, the
virus requires mediator activity, which is provided by
20 HVEM. HVEM interacts with the virus by binding to the
envelope glycoprotein D (gD) and triggering membrane
fusion (Whitbeck et al. (1997) *J. Virol.* 71:6083-6093;
Montgomery et al., *supra*).

To date, two ligands of HVEM have been identified,
25 LIGHT and Lymphotoxin α (LT α) (Mauri et al. (1998)
Immunity, 8:21-30). LIGHT is a novel cytokine and is
termed LIGHT because it shows homology to Lymphotoxins,
exhibits Inducible expression and competes with HSV
Glycoprotein D for HVEM, a receptor expressed by T
30 lymphocytes. The second identified ligand of HVEM, LT α ,
is expressed exclusively by T-cells, has 30% sequence
identity to TNF, and competes with TNF for binding to the
TNF1 receptor. The biological effects exerted by LT α are
similar to those of TNF. However, unlike TNF, LT α
35 usually acts as a local paracrine factor. LT α has been

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shown to be a potent activator of neutrophils. Accordingly, it is thought to be a regulator of acute phase inflammatory reactions. In addition, LT α facilitates leukocyte extravasation by increasing
5 leukocyte adhesion and cytokine production.

Recent evidence suggests that HVEM may also play a role in regulating immune responses. Studies have revealed that HVEM can bind to several TNF receptor-associated factors (TRAFs). TRAFs activate stress
10 activated protein kinase-1/c-Jun N-terminal kinase (JNK/SAPK), as well as the transcription factors, Nuclear Factor-KAPPA B (NF-kB), and transcription factor activator protein-1 (AP-1). These transcription factors in turn control the expression of multiple immune,
15 inflammatory, and acute phase genes (Marsters et al. (1997) *J. Biol. Chem.* 272:14029-14032).

Summary of the Invention

The present invention is based, at least in part, on the discovery of a gene encoding TANGO-69 (also
20 previously known as FLLM). The murine TANGO-69 cDNA described below encodes a type II membrane protein that is predicted to be the murine homologue of the human HVEM ligand, LIGHT (SEQ ID NO:16) (Mauri et al., *supra*).

The murine TANGO-69 cDNA described below (SEQ ID
25 NO:1) has a 717 nucleotide open reading frame (nucleotides 116-831 of SEQ ID NO:1; SEQ ID NO:3) which encodes a 239 amino acid protein (SEQ ID NO:2). TANGO-69 is predicted to have a predicted intracellular domain from about amino acid 1 to amino acid 95 of SEQ ID NO:2;
30 SEQ ID NO:4; a predicted transmembrane domain from about amino acid 96 to amino acid 112 of SEQ ID NO:2; SEQ ID NO:5; and a predicted extracellular domain from about amino acid 113 to amino acid 239 of SEQ ID No:2; SEQ ID NO:6. The region of TANGO-69 from amino acid 91 to amino

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acid 239 (SEQ ID NO:7) has homology to the TNFR-ligand superfamily.

The TANGO-69 molecules of the present invention are useful as modulating agents in regulating a variety of cellular processes. TANGO-69 may bind directly to the membrane-bound form of HVEM (mHVEM) and may act as a natural inhibitor of mHVEM activity, or as a natural activator of mHVEM activity. Alternatively, TANGO-69 may bind directly to soluble HVEM (also known as TANGO-69-receptor, see U.S. serial number _____, filed _____, hereby incorporated by reference) and may regulate the binding of TANGO-69-receptor to mHVEM. For example, the binding of TANGO-69 to the TANGO-69-receptor may inhibit the binding of TANGO-69-receptor to mHVEM.

Alternatively, the binding of TANGO-69 to TANGO-69-receptor may alter TANGO-69 activity by modulating a TANGO-69 signaling pathway. Alternatively, TANGO-69 may bind to other molecules in the mHVEM signalling pathway, thereby inhibiting or activating mHVEM.

TANGO-69 may play a crucial role in inhibiting inflammation, cell proliferation, or viral infection in situations where TANGO-69 either : (a) inhibits TANGO-69-receptor activity by preventing the binding TANGO-69-receptor to mHVEM or (b) inhibits mHVEM activity by binding directly to mHVEM. Alternatively, if TANGO-69 activates mHVEM activity by either : (a) directly binding to mHVEM or (b) by binding to the TANGO-69-receptor and activating the TANGO-69-receptor to bind to mHVEM, TANGO-69 may act as an inducer of inflammation, cell proliferation or viral proliferation.

Since TANGO-69 is a member of the TNFR-ligand superfamily, TANGO-69 may have a role analogous to other members of the superfamily. For example, TANGO-69 may play a role in programmed cell death and apoptosis.

In situ expression analysis revealed that murine TANGO-69 is expressed almost exclusively in cells of the

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megakaryocyte lineage. This very specific expression pattern suggests that TANGO-69 may play an important role in platelet/endothelium interactions. TANGO-69 is able to upregulate the expression of vascular endothelial
5 adhesion surface proteins such as E-selectin and VCAM (see Example 9). These adhesion molecules are involved in mediating the attachment of circulating leukocytes to endothelial cells. Furthermore, TANGO-69 causes
10 The secreted chemokines can bind to the endothelial cell surface heparan sulfate glycosaminoglycans, where they interact with the bound lymphocytes and trigger leukocyte extravasation. These results suggest that TANGO-69 is involved in initiating and regulating the inflammatory
15 response in endothelial cells

In situations associated with aberrant inflammation of endothelial cells, TANGO-69 may be continuously produced and cause persistent low grade damage to the vascular endothelium resulting in abnormal
20 tissue injury and repair. Thus, TANGO-69 may play a critical role in regulating coagulation and may also be involved in regulating tumour growth. Additionally, TANGO-69 may play a role in the pathogenesis of vascular infarctions and arteriosclerotic lesions.

25 TANGO-69 has the ability to bind mast cells (see Example 8). Thus TANGO-69 may be involved in activating mast cells, for example, TANGO-69 may be involved in regulating the secretion of pre-formed granules from the mast cell, thereby regulating the synthesis of lipid
30 precursors (e.g., prostaglandins) in mast cells and regulating the expression and secretion of cytokines from mast cells. Alternatively, TANGO-69 may inhibit the activity of mast cells. Since mast cells play a pathological role in some disease processes, for example
35 delayed hypersensitivity reactions, fibrosis, autoimmune pathology, neoplasia, inflammation in the rheumatoid

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synovium and inflammatory bowel disease, TANGO-69 may be a critical modulator of these disease processes.

In addition, the expression of TANGO-69 in certain cells has been shown to upregulate the production of IL-4 in response to anti-CD3 (see Example 10). IL-4 is itself required for the production of IgE as it stimulates the switching of B cells to IgE production. IgE is the principle mediator of immediate hypersensitivity (allergic) reactions and enhanced production of IL-4 is believed to be central to the development of allergies. Thus, antagonists of TANGO-69 or antibodies directed against TANGO-69 may be important in regulating allergic reactions and may be useful in the treatment of asthma, allograft rejection and other disorders involving an allergic response.

Accordingly, in one aspect, this invention provides isolated nucleic acid molecules encoding TANGO-69 proteins or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection of TANGO-69-encoding nucleic acids.

The invention features a nucleic acid molecule which is at least 50% (or 55%, 65%, 75%, 85%, 95%, or 98%) identical to the nucleotide sequence shown in SEQ ID NO:1, or SEQ ID NO:3, or the nucleotide sequence of the cDNA insert of the plasmid deposited with ATCC as Accession Number (the "cDNA of ATCC 98496"), or a complement thereof.

The invention features a nucleic acid molecule which includes a fragment of at least 300 (325, 350, 375, 400, 425, 450, 500, 550, 600, 650, 700, 800, 900, 1000, 1300, 1600, or 1894) nucleotides of the nucleotide sequence shown in SEQ ID NO:1, or SEQ ID NO:3, or the nucleotide sequence of the cDNA ATCC 98496, or a complement thereof.

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The invention also features a nucleic acid molecule which includes a nucleotide sequence encoding a protein having an amino acid sequence that is at least 78% (or 80%, 85%, 95%, or 98%) identical to the amino acid sequence of SEQ ID NO:2, or the amino acid sequence encoded by the cDNA of ATCC 98496.

In a preferred embodiment, a TANGO-69 nucleic acid molecule has the nucleotide sequence shown SEQ ID NO:1, SEQ ID NO:3, or the nucleotide sequence of the cDNA of ATCC 98496.

Also within the invention is a nucleic acid molecule which encodes a fragment of a polypeptide having the amino acid sequence of SEQ ID NO:2, the fragment including at least 15 (25, 30, 50, 100, 150, 239) contiguous amino acids of SEQ ID NO:2 or the polypeptide encoded by the cDNA of ATCC Accession Number 98496.

The invention includes a nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an amino acid sequence encoded by the cDNA of ATCC Accession Number 98496, wherein the nucleic acid molecule hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3 or a complement thereof under stringent conditions.

Also within the invention are: an isolated TANGO-69 protein having an amino acid sequence that is at least about 78%, preferably 80%, 85%, 95%, or 98% identical to the amino acid sequence of SEQ ID NO:2; an isolated TANGO-69 protein having an amino acid sequence that is at least about 85%, 95%, or 98% identical to the intracellular domain of SEQ ID NO:2 (e.g., about amino acid residues 1 to 95 of SEQ ID NO:2; SEQ ID NO:4); an isolated TANGO-69 protein having an amino acid sequence that is at least about 85%, 95%, or 98% identical to the transmembrane domain of SEQ ID NO:2 (e.g., about amino acid residues 96 to 112 of SEQ ID NO:2; SEQ ID NO:5); and

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an isolated TANGO-69 protein having an amino acid sequence that is at least about 85%, 95%, or 98% identical to the extracellular domain of SEQ ID NO:2 (e.g., about amino acid residues 113 to 239 of SEQ ID NO:2; SEQ ID NO:6). Also within the invention are: an isolated TANGO-69 protein which is encoded by a nucleic acid molecule having a nucleotide sequence that is at least about 65%, preferably 75%, 85%, or 95% identical to SEQ ID NO:3 or the cDNA of ATCC 98496; an isolated TANGO-69 protein which is encoded by a nucleic acid molecule having a nucleotide sequence at least about 65%, preferably 75%, 85%, or 95% identical to the intracellular domain encoding portion of SEQ ID NO:1 (e.g., about nucleotides 116 to 399 of SEQ ID NO:1, SEQ ID NO:8); an isolated TANGO-69 protein which is encoded by a nucleic acid molecule having a nucleotide sequence at least about 65%, preferably 75%, 85%, or 95% identical to the transmembrane domain encoding portion of SEQ ID NO:1 (e.g., about nucleotides 400 to 450 of SEQ ID NO:1; SEQ ID NO:9); and an isolated TANGO-69 protein which is encoded by a nucleic acid molecule having a nucleotide sequence at least about 65%, preferably 75%, 85%, or 95% identical to the extracellular domain encoding portion of SEQ ID NO:1 (e.g., about nucleotides 451 to 831 of SEQ ID NO:1; SEQ ID NO:10); and an isolated TANGO-69 protein which is encoded by a nucleic acid molecule having a nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:3, its complement or the non-coding strand of the cDNA of ATCC 98496.

Also within the invention is a polypeptide which is a naturally occurring allelic variant of a polypeptide that includes the amino acid sequence of SEQ ID NO:2 or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496,

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wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3 or a complement thereof under stringent conditions;

5 Another embodiment of the invention features TANGO-69 nucleic acid molecules which specifically detect TANGO-69 nucleic acid molecules relative to nucleic acid molecules encoding other members of the TNFR-ligand superfamily. For example, in one embodiment, a TANGO-69
10 nucleic acid molecule hybridizes under stringent conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA of ATCC 98496, or a complement thereof. In another embodiment, the TANGO-69 nucleic acid molecule is at
15 least 300 (325, 350, 375, 400, 425, 450, 500, 550, 600, 650, 700, 800, 900, 1000, 1300, 1600, or 2000) nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3,
20 the cDNA of ATCC 98496, or a complement thereof. In a preferred embodiment, an isolated TANGO-69 nucleic acid molecule comprises nucleotides 116 to 399 of SEQ ID NO:1; SEQ ID NO:8, encoding the intracellular domain of TANGO-69, or a complement thereof. In yet another preferred
25 embodiment, an isolated TANGO-69 nucleic acid molecule comprises nucleotides 400 to 450 of SEQ ID NO:1; SEQ ID NO:9, encoding the transmembrane domain of TANGO-69, or a complement thereof. In still yet another preferred embodiment, an isolated TANGO-69 nucleic acid molecule
30 comprises nucleotides 451 to 831 of SEQ ID NO:1; SEQ ID NO:10, encoding the extracellular domain of TANGO-69, or a complement thereof. In another embodiment, the invention provides an isolated nucleic acid molecule which is antisense to the coding strand of a TANGO-69
35 nucleic acid.

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Another aspect of the invention provides a vector, e.g., a recombinant expression vector, comprising a TANGO-69 nucleic acid molecule of the invention. In another embodiment the invention provides a host cell
5 containing such a vector. The invention also provides a method for producing TANGO-69 protein by culturing, in a suitable medium, a host cell of the invention containing a recombinant expression vector such that a TANGO-69 protein is produced.

10 Another aspect of this invention features isolated or recombinant TANGO-69 proteins and polypeptides. Preferred TANGO-69 proteins and polypeptides possess at least one biological activity possessed by naturally occurring human TANGO-69, e.g., (1) the ability to form
15 protein:protein interactions with proteins in the TANGO-69 signalling pathway; (2) the ability to bind TANGO-69-receptor; (3) the ability to interact with mHVEM, and (4) the ability to bind mast cells. Other activities include: (1) the ability to modulate inflammation, (2)
20 the ability to modulate cytokine production, (3) the ability to modulate leukocyte activation, (4) the ability to modulate MHC I induction, (5) the ability to modulate allergic reactions, (6) the ability to modulate cellular differentiation, (7) the ability to modulate viral
25 proliferation, (8) the ability to modulate cell death, (9) the ability to modulate adhesion molecule induction on endothelial cells and (10) the ability to modulate coagulation.

The TANGO-69 proteins of the present invention, or
30 biologically active portions thereof, can be operably linked to a non-TANGO-69 polypeptide (e.g., heterologous amino acid sequences) to form TANGO-69 fusion proteins. The invention further features antibodies that specifically bind TANGO-69 proteins, such as monoclonal
35 or polyclonal antibodies. In addition, the TANGO-69 proteins or biologically active portions thereof can be

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incorporated into pharmaceutical compositions, which optionally include pharmaceutically acceptable carriers.

In another aspect, the present invention provides a method for detecting the presence of TANGO-69 activity
5 or expression in a biological sample by contacting the biological sample with an agent capable of detecting an indicator of TANGO-69 activity such that the presence of TANGO-69 activity is detected in the biological sample.

In another aspect, the invention provides a method
10 for modulating TANGO-69 activity comprising contacting a cell with an agent that modulates (inhibits or stimulates) TANGO-69 activity or expression such that TANGO-69 activity or expression in the cell is modulated. In one embodiment, the agent is an antibody that
15 specifically binds to TANGO-69 protein. In another embodiment, the agent modulates expression of TANGO-69 by modulating transcription of a TANGO-69 gene, splicing of a TANGO-69 mRNA, or translation of a TANGO-69 mRNA. In yet another embodiment, the agent is a nucleic acid
20 molecule having a nucleotide sequence that is antisense to the coding strand of the TANGO-69 mRNA or the TANGO-69 gene.

In one embodiment, the methods of the present invention are used to treat a subject having a disorder
25 characterized by aberrant TANGO-69 protein activity or nucleic acid expression by administering an agent which is a TANGO-69 modulator to the subject. In one embodiment, the TANGO-69 modulator is a TANGO-69 protein. In another embodiment, the TANGO-69 modulator is a TANGO-
30 69 nucleic acid molecule. In other embodiments, the TANGO-69 modulator is a peptide, peptidomimetic, or other small molecule. In a preferred embodiment, the disorder characterized by aberrant TANGO-69 protein or nucleic acid expression is allergic diseases, or angiogenesis.

35 The present invention also provides a diagnostic assay for identifying the presence or absence of a

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genetic lesion or mutation characterized by at least one of: (i) aberrant modification or mutation of a gene encoding a TANGO-69 protein; (ii) mis-regulation of a gene encoding a TANGO-69 protein; and (iii) aberrant post-translational modification of a TANGO-69 protein, wherein a wild-type form of the gene encodes a protein with a TANGO-69 activity.

In another aspect, the invention provides a method for identifying a compound that binds to or modulates the activity of a TANGO-69 protein. In general, such methods entail measuring a biological activity of a TANGO-69 protein in the presence and absence of a test compound and identifying those compounds which alter the activity of the TANGO-69 protein.

The invention also features methods for identifying a compound which modulates the expression of TANGO-69 by measuring the expression of TANGO-69 in the presence and absence of a compound.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

Brief Description of the Drawings

Figure 1 depicts the cDNA sequence (SEQ ID NO:1) and predicted amino acid sequence (SEQ ID NO:2) of murine TANGO-69 (also referred to as "LIGHT"). The open reading frame of SEQ ID NO:1 extends from nucleotide 116 to nucleotide 831 (SEQ ID NO:3).

Figure 2 depicts an alignment of the amino acid sequence of human Fas ligand (huFASL; Genbank accession number P48023; SEQ ID NO:11), mouse Fas ligand (muFASL; Genbank accession number P41047; SEQ ID NO:12), TANGO-69 (muFLLM; SEQ ID NO:2); human Lymphotoxin (huLT; Genbank accession number Q06643; SEQ ID NO:13), human tumor necrosis factor (huTNF α ; Genbank accession number P01375;

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SEQ ID NO:14) and human APO-2 ligand (huAPO-2L; Genbank accession number P50591; SEQ ID NO:15).

Figure 3 depicts an alignment of the amino acid sequence of TANGO-69 (mT69; SEQ ID NO:2) with human LIGHT (LIGHT; Genbank accession number AF036581; SEQ ID NO:16).

Figure 4 is a hydropathy plot of TANGO-69.

Detailed Description of the Invention

The present invention is based on the discovery of a cDNA molecule encoding mouse TANGO-69, a member of the tumour necrosis ligand superfamily. A nucleotide sequence encoding a murine TANGO-69 protein is shown in Figure 1 (SEQ ID NO:1; SEQ ID NO:3 includes the open reading frame only). A predicted amino acid sequence of TANGO-69 protein is also shown in Figure 1 (SEQ ID NO: 2).

The TANGO-69 cDNA of Figure 1 (SEQ ID NO:1), which is approximately 1894 nucleotides long including untranslated regions, encodes a protein amino acid having a molecular weight of approximately 26.3 kDa (excluding post-translational modifications). A plasmid containing a cDNA encoding human TANGO-69 (with the cDNA insert name of _____) was deposited with American Type Culture Collection (ATCC), Manassas, Virginia on July 11, 1997 and assigned Accession Number 98496. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. This deposit was made merely as a convenience for those of skill in the art and is not an admission that a deposit is required under 35 U.S.C. 112.

Alignment of murine TANGO-69 (SEQ ID NO:2) with human Fas ligand (huFASL; Genbank accession number P48023; SEQ ID NO:11) revealed 30% identity at the nucleotide level and 54% identity at the amino acid level (see Figure 2). TANGO-69 is predicted to be the mouse homologue of the human HVEM ligand, LIGHT. An alignment

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of murine TANGO-69 (SEQ ID NO:2) with LIGHT (Genbank accession number AF036581; SEQ ID NO:16) revealed 48% identity at the nucleotide level and 77% identity at the amino acid level (see Figure 3).

5 *In situ* hybridisation revealed that a TANGO-69 mRNA transcript is present in the liver of embryonic mice on day 12.5, 13.5, 14.5 16.5 and postnatal day 1.5. TANGO-69 mRNA expression was also detected in megakaryocytes and myeloid cells.

10 Northern analysis was used to examine TANGO-69 expression. Murine Northern analysis revealed that TANGO-69 is expressed as an approximate 2 kb transcript in the spleen and lung and as an approximate 1.4 kb transcript in heart and skeletal muscle. Human Northern
15 blots purchased from Clontech (Palo Alto, CA) were also probed with TANGO-69 and a TANGO-69 mRNA transcript was also detected in the same tissues as in the mice, i.e., spleen, lung, heart and skeletal muscle.

 Murine TANGO-69 is one member of a family of
20 molecules (the "TANGO-69 family") having certain conserved structural and functional features. The term "family" when referring to the protein and nucleic acid molecules of the invention is intended to mean two or more proteins or nucleic acid molecules having a common
25 structural domain and having sufficient amino acid or nucleotide sequence identity as defined herein. Such family members can be naturally occurring and can be from either the same or different species. For example, a family can contain a first protein of human origin and a
30 homologue of that protein of murine origin, as well as a second, distinct protein of human origin and a murine homologue of that protein. Members of a family may also have common functional characteristics.

 In one embodiment, a TANGO-69 protein includes a
35 intracellular domain having at least about 80%, preferably at least about 85%, and more preferably about

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95%, or 98% amino acid sequence identity to the intracellular domain of SEQ ID NO:4. In another embodiment, a TANGO-69 protein includes a transmembrane domain having at least about 80, preferably at least
5 about 85%, and more preferably about 95%, or 98% amino acid sequence identity to the transmembrane domain of SEQ ID NO:5. In yet another embodiment, a TANGO-69 protein includes a extracellular domain having at least about 80%, preferably at least about 85%, and more preferably
10 about 95%, or 98% amino acid sequence identity to the extracellular domain of SEQ ID NO:6.

Preferred TANGO-69 polypeptides of the present invention have an amino acid sequence sufficiently identical to the amino acid sequence of the intracellular
15 domain (SEQ ID NO:4), the amino acid sequence of the transmembrane domain (SEQ ID NO:5) and the amino acid sequence of extracellular domain (SEQ ID NO:6). As used herein, the term "sufficiently identical" refers to a first amino acid or nucleotide sequence which contains a
20 sufficient or minimum number of identical or equivalent (e.g., with a similar side chain) amino acid residues or nucleotides to a second amino acid or nucleotide sequence such that the first and second amino acid or nucleotide sequences have a common structural domain and/or common
25 functional activity. For example, amino acid or nucleotide sequences which contain a common structural domain having about 80% identity, preferably 85% identity, more preferably 95%, or 98% identity are defined herein as sufficiently identical.

30 As used interchangeably herein a "TANGO-69 activity", "biological activity of TANGO-69" or "functional activity of TANGO-69", refers to an activity exerted by a TANGO-69 protein, polypeptide or nucleic acid molecule on a TANGO-69 responsive cell as determined
35 *in vivo*, or *in vitro*, according to standard techniques. A TANGO-69 activity can be a direct activity, such as an

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association with or an enzymatic activity on a second protein or an indirect activity, such as a cellular signaling activity mediated by interaction of the TANGO-69 protein with a second protein. In a preferred embodiment, a TANGO-69 activity includes at least one or more of the activities described herein.

Accordingly, another embodiment of the invention features isolated TANGO-69 proteins and polypeptides having a TANGO-69 activity.

Various aspects of the invention are described in further detail in the following subsections.

I. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode TANGO-69 proteins or biologically active portions thereof, as well as nucleic acid molecules sufficient for use as hybridization probes to identify TANGO-69-encoding nucleic acids (e.g., TANGO-69 mRNA) and fragments for use as PCR primers for the amplification or mutation of TANGO-69 nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences (preferably protein encoding sequences) which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the

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isolated TANGO-69 nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or the cDNA of ATCC 98496, or a complement of any of these nucleotide sequences, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:3, or the cDNA of ATCC 98496 as a hybridization probe, TANGO-69 nucleic acid molecules can be isolated using standard hybridization and cloning techniques (e.g., as described in Sambrook et al., eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

A nucleic acid of the invention can be amplified using cDNA, mRNA or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to TANGO-69 nucleotide sequences can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a

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nucleic acid molecule which is a complement of the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, or the cDNA of ATCC 98496, or a portion thereof. A nucleic acid molecule which is complementary to a given
5 nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize to the given nucleotide sequence thereby forming a stable duplex.

Moreover, the nucleic acid molecule of the
10 invention can comprise only a portion of a nucleic acid sequence encoding TANGO-69, for example, a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of TANGO-69. The nucleotide sequence determined from the cloning of the murine TANGO-
15 69 gene allows for the generation of probes and primers designed for use in identifying and/or cloning TANGO-69 homologues in other cell types, e.g., from other tissues, as well as TANGO-69 homologues from other mammals. The probe/primer typically comprises substantially purified
20 oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 50, 75, 100, 125, 150, 175, 200, 250, 300, 350 or 400 consecutive nucleotides of
25 the sense or anti-sense sequence of SEQ ID NO:1, SEQ ID NO:3 or the cDNA of ATCC 98496 or of a naturally occurring mutant of SEQ ID NO:1, SEQ ID NO:3, or the cDNA of ATCC 98496.

Probes based on the murine TANGO-69 nucleotide
30 sequence can be used to detect transcripts or genomic sequences encoding the same or identical proteins. The probe comprises a label group attached thereto, e.g., a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a
35 diagnostic test kit for identifying cells or tissues which mis-express a TANGO-69 protein, such as by

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measuring levels of a TANGO-69-encoding nucleic acid in a sample of cells from a subject, e.g., detecting TANGO-69 mRNA levels or determining whether a genomic TANGO-69 gene has been mutated or deleted.

5 A nucleic acid fragment encoding a "biologically active portion of TANGO-69" can be prepared by isolating a portion of SEQ ID NO:1, SEQ ID NO:3, or the nucleotide sequence of the cDNA of ATCC 98496 which encodes a polypeptide having a TANGO-69 biological activity,
10 expressing the encoded portion of TANGO-69 protein (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of TANGO-69. For example, a nucleic acid fragment encoding a biologically active portion of TANGO-69 includes an extracellular
15 domain, e.g., SEQ ID NO:6.

 The invention further encompasses nucleic acid molecules that differ from the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or the cDNA of ATCC 98496 due to degeneracy of the genetic code and thus encode the same
20 TANGO-69 protein as that encoded by the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, or the nucleotide sequence of the cDNA of ATCC 98496.

 In addition to the murine TANGO-69 nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, or the cDNA
25 of ATCC 98496, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of TANGO-69 may exist within a population (e.g., the murine population). Such genetic polymorphism in the TANGO-69 gene may exist among
30 individuals within a population due to natural allelic variation. An allele is one of a group of genes which occur alternatively at a given genetic locus. As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a TANGO-69 locus or
35 to a polypeptide encoded by the nucleotide sequence. As used herein, the terms "gene" and "recombinant gene"

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refer to nucleic acid molecules comprising an open reading frame encoding a TANGO-69 protein, preferably a mammalian TANGO-69 protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the TANGO-69 gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations in TANGO-69 that are the result of natural allelic variation and that do not alter the functional activity of TANGO-69 are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding TANGO-69 proteins from other species (TANGO-69 homologues), which have a nucleotide sequence which differs from that of murine TANGO-69, are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the TANGO-69 cDNA of the invention can be isolated based on their identity to the murine TANGO-69 nucleic acids disclosed herein using the murine cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. For example, a soluble murine TANGO-69 cDNA can be isolated based on its identity to murine membrane-bound TANGO-69. Likewise, a cDNA encoding a membrane-bound form of murine TANGO-69 can be isolated based on its identity to soluble murine TANGO-69.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 300 (325, 350, 375, 400, 425, 450, 500, 550, 600, 650, 700, 800, 900, 1000, or 1290) nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence, preferably

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the coding sequence, of SEQ ID NO:1, SEQ ID NO:3, the cDNA of ATCC 98496, or a complement thereof.

As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% (65%, 70%, preferably 75%) identical to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA of ATCC 98496, or the complement thereof, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In addition to naturally-occurring allelic variants of the TANGO-69 sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or the cDNA of ATCC 98496, thereby leading to changes in the amino acid sequence of the encoded TANGO-69 protein, without altering the biological activity of the TANGO-69 protein. For example, nucleotide substitutions can be made which lead to amino acid substitutions at "non-essential" amino acid residues. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of TANGO-69 (e.g., the sequence of SEQ

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ID NO:2) without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are not conserved or only semi-conserved among
5 TANGO-69 of various species may be non-essential for activity and thus would be likely targets for alteration. Alternatively, amino acid residues that are conserved among the TANGO-69 proteins of various species may be essential for activity and thus would not be likely
10 targets for alteration.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding TANGO-69 proteins that contain changes in amino acid residues that are not essential for activity. Such TANGO-69 proteins
15 differ in amino acid sequence from SEQ ID NO:2 yet retain biological activity. In one embodiment, the isolated nucleic acid molecule includes a nucleotide sequence encoding a protein that includes an amino acid sequence that is at least about 45% identical, 65%, 75%, 85%, 95%,
20 or 98% identical to the amino acid sequence of SEQ ID NO:2.

An isolated nucleic acid molecule encoding a TANGO-69 protein having a sequence which differs from that of SEQ ID NO:2 can be created by introducing one or
25 more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA of ATCC 98496 such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced by
30 standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A
"conservative amino acid substitution" is one in which
35 the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino

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acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in TANGO-69 is preferably replaced with another amino acid residue from the same side chain family. Alternatively, mutations can be introduced randomly along all or part of a TANGO-69 coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for TANGO-69 biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

In a preferred embodiment, a mutant TANGO-69 protein can be assayed for: (1) the ability to form protein:protein interactions with proteins in the TANGO-69 signalling pathway; (2) the ability to bind TANGO-69-receptor; (3) the ability to interact with mHVEM, and (4) the ability to bind mast cells. Other activities include: (1) the ability to modulate inflammation, (2) the ability to modulate cytokine production, (3) the ability to modulate leukocyte activation, (4) the ability to modulate MHC I induction, (5) the ability to modulate allergic reactions, (6) the ability to modulate cellular differentiation, (7) the ability to modulate viral proliferation, (8) the ability to modulate of cell death, (9) the ability to modulate adhesion molecule induction

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on endothelial cells, and (10) ability to modulate coagulation.

The present invention encompasses antisense nucleic acid molecules, i.e., molecules which are
5 complementary to a sense nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense
10 nucleic acid can be complementary to an entire TANGO-69 coding strand, or to only a portion thereof, e.g., all or part of the protein coding region (or open reading frame). An antisense nucleic acid molecule can be antisense to a noncoding region of the coding strand of a
15 nucleotide sequence encoding TANGO-69. The noncoding regions ("5' and 3' untranslated regions") are the 5' and 3' sequences which flank the coding region and are not translated into amino acids.

Given the coding strand sequences encoding TANGO-
20 69 disclosed herein (e.g., SEQ ID NO:1 or SEQ ID NO:3), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of TANGO-69 mRNA, but more
25 preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of TANGO-69 mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of TANGO-69 mRNA,
30 e.g., an oligonucleotide having the sequence
CCCGAGGCCTCGGAGTCGACGAGACCGTACCTC (SEQ ID NO:19) or
TCGACGAGACCGTACCTCTCACACCATY (SEQ ID NO:20). An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in
35 length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic

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ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously
5 modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

10 Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-
15 carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-
20 methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid
25 (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil,
30 (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an
35 antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a TANGO-69 protein to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier et al. (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue et al.

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(1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al. (1987) *FEBS Lett.* 215:327-330).

The invention also encompasses ribozymes.

5 Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988)
10 *Nature* 334:585-591)) can be used to catalytically cleave TANGO-69 mRNA transcripts to thereby inhibit translation of TANGO-69 mRNA. A ribozyme having specificity for a TANGO-69-encoding nucleic acid can be designed based upon the nucleotide sequence of a TANGO-69 cDNA disclosed
15 herein (e.g., SEQ ID NO:1, SEQ ID NO:3). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a TANGO-69-encoding mRNA. See, e.g.,
20 Cech et al. U.S. Patent No. 4,987,071; and Cech et al. U.S. Patent No. 5,116,742. Alternatively, TANGO-69 mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel and Szostak (1993) *Science* 261:1411-1418.

25 The invention also encompasses nucleic acid molecules which form triple helical structures. For example, TANGO-69 gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the TANGO-69 (e.g., the TANGO-69
30 promoter and/or enhancers) to form triple helical structures that prevent transcription of the TANGO-69 gene in target cells. See generally Helene (1991) *Anticancer Drug Des.* 6(6):569-84; Helene (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays*
35 14(12):807-15.

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In preferred embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) *Bioorganic & Medicinal Chemistry* 4(1): 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996), *supra*; Perry-O'Keefe et al. (1996) *Proc. Natl. Acad. Sci. USA* 93: 14670-675.

PNAs of TANGO-69 can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of TANGO-69 can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup (1996), *supra*; or as probes or primers for DNA sequence and hybridization (Hyrup (1996), *supra*; Perry-O'Keefe et al. (1996) *Proc. Natl. Acad. Sci. USA* 93: 14670-675).

In another embodiment, PNAs of TANGO-69 can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use

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of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of TANGO-69 can be generated which may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA
5 recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking,
10 number of bonds between the nucleobases, and orientation (Hyrup (1996), *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), *supra*, and Finn et al. (1996) *Nucleic Acids Res.* 24(17):3357-63. For example, a DNA chain can be synthesized on a solid
15 support using standard phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can be used as a link between the PNA and the 5' end of DNA (Mag et al. (1989) *Nucleic Acids Res.* 17:5973-88).
20 PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) *Nucleic Acids Res.* 24(17):3357-63). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment
25 (Peterser et al. (1975) *Bioorganic Med. Chem. Lett.* 5:1119-11124).

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents
30 facilitating transport across the cell membrane (*see*, e.g., Letsinger et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:648-652; PCT Publication No. W0 88/09810) or the blood-brain barrier (*see*, e.g., PCT Publication No.
35 W0 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents

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(see, e.g., Krol et al. (1988) *Bio/Techniques* 6:958-976) or intercalating agents (see, e.g., Zon (1988) *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide,
5 hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

II. Isolated TANGO-69 Proteins and Anti-TANGO-69 Antibodies

One aspect of the invention pertains to isolated
10 TANGO-69 proteins, and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise anti-TANGO-69 antibodies. In one embodiment, native TANGO-69 proteins can be isolated from cells or tissue sources by an appropriate
15 purification scheme using standard protein purification techniques. In another embodiment, TANGO-69 proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a TANGO-69 protein or polypeptide can be synthesized chemically using standard peptide
20 synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the TANGO-69 protein
25 is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of TANGO-69 protein in which the protein is separated from cellular components of the
30 cells from which it is isolated or recombinantly produced. Thus, TANGO-69 protein that is substantially free of cellular material includes preparations of TANGO-69 protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of non-TANGO-69 protein (also referred to
35 herein as a "contaminating protein"). When the TANGO-69

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protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When TANGO-69 protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, i.e., it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such preparations of TANGO-69 protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or non-TANGO-69 chemicals.

Biologically active portions of a TANGO-69 protein include peptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the TANGO-69 protein (e.g., the amino acid sequence shown in SEQ ID NO:2), which include fewer amino acids than the full length TANGO-69 proteins, and exhibit at least one activity of a TANGO-69 protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the TANGO-69 protein. A biologically active portion of a TANGO-69 protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native TANGO-69 protein.

Preferred TANGO-69 protein has the amino acid sequence shown of SEQ ID NO:2. Other useful TANGO-69 proteins are substantially identical to SEQ ID NO:2 and retain the functional activity of the protein of SEQ ID NO:2 yet differ in amino acid sequence due to natural allelic variation or mutagenesis. TANGO-69 can play a role in inflammation, e.g., TANGO-69 has the ability to

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modulate cytokine production, the ability to modulate leukocyte activation, the ability to modulate MHC I induction, the ability to modulate expression of adhesion proteins and the ability to modulate allergic reactions.

5 TANGO-69 can play a role in vascular diseases, e.g., TANGO-69 has the ability to modulate angiogenesis, the ability to modulate vascular infarctions, and the ability to modulate the formation of arteriosclerotic lesions. TANGO-69 can play a role in HSV pathogenesis, e.g.,

10 TANGO-69 has the ability to modulate the entry of HSV into cells. TANGO-69 can play a role in cellular differentiation and cell death. TANGO-69 can also play a role in coagulation. Accordingly, a useful TANGO-69 protein is a protein which includes an amino acid

15 sequence at least about 45%, preferably 55%, 65%, 75%, 80%, 85%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:2 and retains the functional activity of the TANGO-69 proteins of SEQ ID NO:2. In a preferred embodiment, the TANGO-69 protein retains a

20 functional activity of the TANGO-69 protein of SEQ ID NO:2.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can

25 be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position

30 in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical

35 positions shared by the sequences (i.e., % identity = # of identical positions/total # of positions (e.g.,

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overlapping positions) x 100). Preferably, the two sequences are the same length.

The determination of percent identity between two sequences can be accomplished using a mathematical
5 algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*
10 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous
15 to TANGO-69 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to TANGO-69 protein molecules of the invention. To obtain gapped alignments for comparison
20 purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997) *Nucleic Acids Res.* 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST,
25 and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the
30 algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue
35 table, a gap length penalty of 12, and a gap penalty of 4 can be used.

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The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

5 The invention also provides TANGO-69 chimeric or fusion proteins. As used herein, a TANGO-69 "chimeric protein" or "fusion protein" comprises a TANGO-69 polypeptide operably linked to a non-TANGO-69 polypeptide. A "TANGO-69 polypeptide" refers to a
10 polypeptide having an amino acid sequence corresponding to TANGO-69, whereas a "non-TANGO-69 polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially identical to the TANGO-69 protein, e.g., a protein which
15 is different from the TANGO-69 protein and which is derived from the same or a different organism. Within a TANGO-69 fusion protein the TANGO-69 polypeptide can correspond to all or a portion of a TANGO-69 protein, preferably at least one biologically active portion of a
20 TANGO-69 protein. Within the fusion protein, the term "operably linked" is intended to indicate that the TANGO-69 polypeptide and the non-TANGO-69 polypeptide are fused in-frame to each other. The non-TANGO-69 polypeptide can be fused to the N-terminus or C-terminus of the TANGO-69
25 polypeptide.

One useful fusion protein is a GST-TANGO-69 fusion protein in which the TANGO-69 sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant TANGO-69.

30 In yet another embodiment, the fusion protein is an TANGO-69-immunoglobulin fusion protein in which all or part of TANGO-69 is fused to sequences derived from a member of the immunoglobulin protein family. The TANGO-69-immunoglobulin fusion proteins of the invention can be
35 incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction

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between a TANGO-69 ligand and a TANGO-69 protein on the surface of a cell, to thereby suppress TANGO-69-mediated signal transduction *in vivo*. The TANGO-69-immunoglobulin fusion proteins can be used to affect the bioavailability of a TANGO-69 cognate ligand. Inhibition of the TANGO-69 ligand/TANGO-69 interaction may be useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (e.g., promoting or inhibiting) cell survival. Moreover, the TANGO-69-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-TANGO-69 antibodies in a subject, to purify TANGO-69 ligands and in screening assays to identify molecules which inhibit the interaction of TANGO-69 with a TANGO-69 ligand.

Preferably, a TANGO-69 chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, e.g., Ausubel et al., *supra*). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). An TANGO-69-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is

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linked in-frame to the TANGO-69 protein.

The present invention also pertains to variants of the TANGO-69 proteins (i.e., proteins having a sequence which differs from that of the TANGO-69 amino acid
5 sequence). Such variants can function as either TANGO-69 agonists (mimetics) or as TANGO-69 antagonists. Variants of the TANGO-69 protein can be generated by mutagenesis, e.g., discrete point mutation or truncation of the TANGO-69 protein. An agonist of the TANGO-69 protein can retain
10 substantially the same, or a subset, of the biological activities of the naturally occurring form of the TANGO-69 protein. An antagonist of the TANGO-69 protein can inhibit one or more of the activities of the naturally occurring form of the TANGO-69 protein by, for example,
15 competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the TANGO-69 protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. Treatment of a subject with a variant having a subset of
20 the biological activities of the naturally occurring form of the protein can have fewer side effects in a subject relative to treatment with the naturally occurring form of the TANGO-69 proteins.

Variants of the TANGO-69 protein which function as
25 either TANGO-69 agonists (mimetics) or as TANGO-69 antagonists can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the TANGO-69 protein for TANGO-69 protein agonist or antagonist activity. In one embodiment, a variegated
30 library of TANGO-69 variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of TANGO-69 variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene
35 sequences such that a degenerate set of potential TANGO-69 sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g.,

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- for phage display) containing the set of TANGO-69 sequences therein. There are a variety of methods which can be used to produce libraries of potential TANGO-69 variants from a degenerate oligonucleotide sequence.
- 5 Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences
- 10 encoding the desired set of potential TANGO-69 sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) *Tetrahedron* 39:3; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477).

- In addition, libraries of fragments of the TANGO-69 protein coding sequence can be used to generate a variegated population of TANGO-69 fragments for screening and subsequent selection of variants of a TANGO-69
- 20 protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a TANGO-69 coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA,
- 25 renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By
- 30 this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the TANGO-69 protein.

- Several techniques are known in the art for screening gene products of combinatorial libraries made by point
- 35 mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene

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libraries generated by the combinatorial mutagenesis of TANGO-69 proteins. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify TANGO-69 variants (Arkin and Yourvan (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave et al. (1993) *Protein Engineering* 6(3):327-331).

An isolated TANGO-69 protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind TANGO-69 using standard techniques for polyclonal and monoclonal antibody preparation. The full-length TANGO-69 protein can be used or, alternatively, the invention provides antigenic peptide fragments of TANGO-69 for use as immunogens. The antigenic peptide of TANGO-69 comprises at least 8 (preferably 10, 15, 20, or 30) amino acid residues of the amino acid sequence shown in SEQ ID NO:2 and encompasses an epitope of TANGO-69 such that an antibody raised against the peptide forms a specific immune complex with TANGO-69.

Preferred epitopes encompassed by the antigenic peptide are regions of TANGO-69 that are located on the surface of the protein, e.g., hydrophilic regions. A hydrophobicity analysis of the murine TANGO-69 protein sequence indicates that the regions between, e.g., amino acids 70 and 95, between amino acids 165 and 180, and between amino acids 218 and 236 of SEQ ID NO:2 are particularly hydrophilic and, therefore, are likely to

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encode surface residues useful for targeting antibody production.

An antigenic TANGO-69 immunogen typically is used to prepare antibodies by immunizing a suitable subject, (e.g., rabbit, goat, mouse or other mammal) with the immunogen. An appropriate immunogenic preparation can contain, for example, antigen recombinantly expressed TANGO-69 protein or a chemically synthesized TANGO-69 polypeptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or similar immunostimulatory agent. Immunization of a suitable subject with an antigenic TANGO-69 preparation induces a polyclonal anti-TANGO-69 antibody response.

The antigenic peptide of TANGO-69 comprises at least 7 (preferably 10, 15, 20, 30, or more) amino acid residues of TANGO-69 (SEQ ID NO:2), and encompasses at least one epitope of TANGO-69 such that an antibody raised against the peptide forms a specific immune complex with TANGO-69. Other preferred immunogens include all or a portion (e.g., a portion which comprises at least 7 amino acid residues) of TANGO-69; e.g., amino acids 39-45, 40-46, 41-47, 42-48, 43-49, 44-50, 45-51, 46-52, 47-53, 48-54, 49-55, 50-56, 51-57, 52-58, 53-59, 54-60, 55-61, 56-62, 57-63, 58-64, 59-65, 60-66, 61-67, 62-68, 63-69, 64-70, 65-71, 66-72, 67-73, 68-74, 69-75, 70-76, 71-77, 72-78, 73-79, 74-80, 75-81, 76-82, 77-83, 78-84, 79-85, 80-86, 81-87, 82-88, 83-89, 84-90, 85-91, 86-92, 87-93, 88-94, 89-95, 90-96, 91-97, 92-98, 93-99, 94-100, 95-101, 96-102, 97-103, 98-104, 99-105, 100-106, 101-107, 102-108, 103-109, 104-110, 105-111, 106-112, 107-113, 108-114, 109-115, 110-116, 111-117, 112-118, 113-119, 114-120, 115-121, 116-122, 117-123, 118-124, 119-125, 120-126, 121-127, 122-128, 123-129, 124-130, 125-131, 126-132, 127-133, 128-134, 129-135, 130-136, 131-137, 132-138, 133-139, 134-140, 135-141, 136-142, 137-143, 138-144, 139-145, 140-146, 141-147, 142-148, 143-149, 144-150, 145-151, 146-152, 147-153, 148-154, 149-155, 150-

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156, 151-157, 152-158, 153-159, 154-160, 155-161, 156-162,
157-163, 158-164, 159-165, 160-166, 161-167, 162-168, 163-
169, 164-170, 165-171, 166-172, 167-173, 168-174, 169-175,
170-176, 171-177, 172-178, 173-179, 174-180, 175-181, 176-
5 182, 177-183, 178-184, 179-185, 180-186, 181-187, 182-188,
183-189, 184-190, 185-191, 186-192, 187-193, 188-194, 189-
195, 190-196, 191-197, 192-198, 193-199, 194-200, 195-201,
196-202, 197-203, 198-204, 199-205, 200-206, 201-207, 202-
208, 203-209, 204-210, 205-211, 206-212, 207-213, 208-214,
10 209-215, 210-216, 211-217, 212-218, 213-219, 214-220, 215-
221, 216-222, 217-223, 218-224, 219-225, 220-226, 221-227,
222-228, 223-229, 224-230, 225-231, 226-232, 227-233, 228-
234, 229-235, 230-236, 231-237, 232-238, and 233-239.

Accordingly, another aspect of the invention pertains
15 to anti-TANGO-69 antibodies. The term "antibody" as used
herein refers to immunoglobulin molecules and
immunologically active portions of immunoglobulin
molecules, i.e., molecules that contain an antigen binding
site which specifically binds an antigen, such as TANGO-
20 69. A molecule which specifically binds to TANGO-69 is a
molecule which binds TANGO-69, but does not substantially
bind other molecules in a sample, e.g., a biological
sample, which naturally contains TANGO-69. Examples of
immunologically active portions of immunoglobulin
25 molecules include F(ab) and F(ab')₂ fragments which can be
generated by treating the antibody with an enzyme such as
pepsin. The invention provides polyclonal and monoclonal
antibodies that bind TANGO-69. The term "monoclonal
antibody" or "monoclonal antibody composition", as used
30 herein, refers to a population of antibody molecules that
contain only one species of an antigen binding site
capable of immunoreacting with a particular epitope of
TANGO-69. A monoclonal antibody composition thus
typically displays a single binding affinity for a
35 particular TANGO-69 protein with which it immunoreacts.

Polyclonal anti-TANGO-69 antibodies can be prepared
as described above by immunizing a suitable subject with a

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TANGO-69 immunogen. The anti-TANGO-69 antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized TANGO-69.

5 If desired, the antibody molecules directed against TANGO-69 can be isolated from the mammal (e.g., from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, e.g., when the
10 anti-TANGO-69 antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B
15 cell hybridoma technique (Kozbor et al. (1983) *Immunol. Today* 4:72), the EBV-hybridoma technique (Cole et al. (1985), *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see
20 generally *Current Protocols in Immunology* (1994) Coligan et al. (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with a TANGO-69 immunogen as described above,
25 and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds TANGO-69.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for
30 the purpose of generating an anti-TANGO-69 monoclonal antibody (see, e.g., *Current Protocols in Immunology*, supra; Galfre et al. (1977) *Nature* 266:55052; R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York,
35 New York (1980); and Lerner (1981) *Yale J. Biol. Med.*, 54:387-402. Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods

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which also would be useful. Typically, the immortal cell line (e.g., a myeloma cell line) is derived from the same mammalian species as the lymphocytes. For example, murine hybridomas can be made by fusing lymphocytes from a mouse
5 immunized with an immunogenic preparation of the present invention with an immortalized mouse cell line, e.g., a myeloma cell line that is sensitive to culture medium containing hypoxanthine, aminopterin and thymidine ("HAT medium"). Any of a number of myeloma cell lines can be
10 used as a fusion partner according to standard techniques, e.g., the P3-NS1/1-Ag4-1, P3-x63-Ag8.653 or Sp2/O-Ag14 myeloma lines. These myeloma lines are available from ATCC. Typically, HAT-sensitive mouse myeloma cells are fused to mouse splenocytes using polyethylene glycol
15 ("PEG"). Hybridoma cells resulting from the fusion are then selected using HAT medium, which kills unfused and unproductively fused myeloma cells (unfused splenocytes die after several days because they are not transformed). Hybridoma cells producing a monoclonal antibody of the
20 invention are detected by screening the hybridoma culture supernatants for antibodies that bind TANGO-69, e.g., using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal anti-TANGO-69 antibody
25 can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with TANGO-69 to thereby isolate immunoglobulin library members that bind TANGO-69. Kits for generating and screening phage display libraries are
30 commercially available (e.g., the Pharmacia Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene SurfZAP™ Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening
35 antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication

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No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al. (1991) *Bio/Technology* 9:1370-1372; Hay et al. (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse et al. (1989) *Science* 246:1275-1281; Griffiths et al. (1993) *EMBO J.* 12:725-734.

Additionally, recombinant anti-TANGO-69 antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better et al. (1988) *Science* 240:1041-1043; Liu et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu et al. (1987) *J. Immunol.* 139:3521-3526; Sun et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura et al. (1987) *Canc. Res.* 47:999-1005; Wood et al. (1985) *Nature* 314:446-449; and Shaw et al. (1988) *J. Natl. Cancer Inst.* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi et al. (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones et al. (1986) *Nature* 321:552-525; Verhoeyan et al. (1988) *Science* 239:1534; and Beidler et al. (1988) *J. Immunol.* 141:4053-4060.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected

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antigen, e.g., all or a portion of TANGO-69. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice
5 rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human
10 antibodies, see Lonberg and Huszar (1995, *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent
15 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

20 Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely
25 human antibody recognizing the same epitope.

First, a non-human monoclonal antibody which binds a selected antigen (epitope), e.g., an antibody which inhibits TANGO-69 activity, is identified. The heavy chain and the light chain of the non-human antibody are
30 cloned and used to create phage display Fab fragments. For example, the heavy chain gene can be cloned into a plasmid vector so that the heavy chain can be secreted from bacteria. The light chain gene can be cloned into a phage coat protein gene so that the light chain can be
35 expressed on the surface of phage. A repertoire (random collection) of human light chains fused to phage is used to infect the bacteria which express the non-human heavy

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chain. The resulting progeny phage display hybrid antibodies (human light chain/non-human heavy chain). The selected antigen is used in a panning screen to select phage which bind the selected antigen. Several
5 rounds of selection may be required to identify such phage. Next, human light chain genes are isolated from the selected phage which bind the selected antigen. These selected human light chain genes are then used to guide the selection of human heavy chain genes as
10 follows. The selected human light chain genes are inserted into vectors for expression by bacteria. Bacteria expressing the selected human light chains are infected with a repertoire of human heavy chains fused to phage. The resulting progeny phage display human
15 antibodies (human light chain/human heavy chain).

Next, the selected antigen is used in a panning screen to select phage which bind the selected antigen. The phage selected in this step display a completely human antibody which recognizes the same epitope
20 recognized by the original selected, non-human monoclonal antibody. The genes encoding both the heavy and light chains are readily isolated and can be further manipulated for production of human antibody. This technology is described by Jespers et al. (1994,
25 *Bio/technology* 12:899-903).

An anti-TANGO-69 antibody (e.g., monoclonal antibody) can be used to isolate TANGO-69 by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-TANGO-69 antibody can
30 facilitate the purification of natural TANGO-69 from cells and of recombinantly produced TANGO-69 expressed in host cells. Moreover, an anti-TANGO-69 antibody can be used to detect TANGO-69 protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the
35 abundance and pattern of expression of the TANGO-69 protein. Anti-TANGO-69 antibodies can be used

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diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the
5 antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish
10 peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein
15 isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive
20 material include ^{125}I , ^{131}I , ^{35}S or ^3H .

III. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding TANGO-69 (or a portion thereof). As used
25 herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated.
30 Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of
35 replication and episomal mammalian vectors). Other

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vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain
5 vectors, expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include
10 such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention
15 comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which
20 is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of
25 the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g.,
30 polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide
35 sequence in many types of host cell and those which direct expression of the nucleotide sequence only in

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certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to
5 be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein
10 (e.g., TANGO-69 proteins, mutant forms of TANGO-69, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of TANGO-69 in prokaryotic or eukaryotic cells, e.g., bacterial cells such as *E.*
15 *coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7
20 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins.
25 Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant
30 protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to
35 enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion

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protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40),
5 pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli*
10 expression vectors include pTrc (Amann et al., (1988) *Gene* 69:301-315) and pET 11d (Studier et al., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89). Target gene expression from the pTrc vector relies on
15 host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host
20 strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host
25 bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of
30 the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada et al. (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried
35 out by standard DNA synthesis techniques.

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In another embodiment, the TANGO-69 expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari et al. (1987) *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz et al. (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corp, San Diego, CA).

Alternatively, TANGO-69 can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith et al. (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman et al. (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook et al., *supra*.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert et al. (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and

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Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji et al. (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund et al. (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to TANGO-69 mRNA. Regulatory sequences operably linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see

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Weintraub et al. (*Reviews - Trends in Genetics*, Vol. 1(1) 1986).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, TANGO-69 protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride coprecipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, et al. (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene

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that encodes a selectable marker (e.g., for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding TANGO-69 or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) TANGO-69 protein. Accordingly, the invention further provides methods for producing TANGO-69 protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding TANGO-69 has been introduced) in a suitable medium such that TANGO-69 protein is produced. In another embodiment, the method further comprises isolating TANGO-69 from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which TANGO-69-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous TANGO-69 sequences have been introduced into their genome or homologous recombinant animals in which endogenous TANGO-69 sequences have been altered. Such animals are useful for studying the function and/or activity of TANGO-69 and for identifying and/or evaluating modulators of TANGO-69 activity. As

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used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of

5 transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal,

10 thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous

15 TANGO-69 gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

20 A transgenic animal of the invention can be created by introducing TANGO-69-encoding nucleic acid into the male pronuclei of a fertilized oocyte, e.g., by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster

25 animal. The TANGO-69 cDNA sequence e.g., that of (SEQ ID NO:1, SEQ ID NO:3, or the cDNA of ATCC 98496) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human TANGO-69 gene, such as a mouse TANGO-69 gene, can be

30 isolated based on hybridization to the human TANGO-69 cDNA and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can

35 be operably linked to the TANGO-69 transgene to direct expression of TANGO-69 protein to particular cells.

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Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 5 4,870,009, U.S. Patent No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Similar methods are used for production of other transgenic animals. A transgenic founder animal can be 10 identified based upon the presence of the TANGO-69 transgene in its genome and/or expression of TANGO-69 mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic 15 animals carrying a transgene encoding TANGO-69 can further be bred to other transgenic animals carrying other transgenes.

To create an homologous recombinant animal, a vector is prepared which contains at least a portion of a TANGO- 20 69 gene (e.g., a human or a non-human homolog of the TANGO-69 gene, e.g., a murine TANGO-69 gene) into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the TANGO-69 gene. In a preferred embodiment, the vector is designed 25 such that, upon homologous recombination, the endogenous TANGO-69 gene is functionally disrupted (i.e., no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the 30 endogenous TANGO-69 gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous TANGO-69 protein). In the homologous recombination vector, the altered portion of 35 the TANGO-69 gene is flanked at its 5' and 3' ends by additional nucleic acid of the TANGO-69 gene to allow for

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homologous recombination to occur between the exogenous TANGO-69 gene carried by the vector and an endogenous TANGO-69 gene in an embryonic stem cell. The additional flanking TANGO-69 nucleic acid is of sufficient length
5 for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see, e.g., Thomas and Capecchi (1987) *Cell* 51:503 for a description of homologous recombination
10 vectors). The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced TANGO-69 gene has homologously recombined with the endogenous TANGO-69 gene are selected (see, e.g., Li et al. (1992) *Cell* 69:915). The selected
15 cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras (see, e.g., Bradley in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed. (IRL, Oxford, 1987) pp. 113-152). A chimeric embryo can then be implanted
20 into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline
25 transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in Bio/Technology* 2:823-829 and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO
30 92/0968, and WO 93/04169.

In another embodiment, transgenic non-human animals can be produced which contain selected systems which allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase
35 system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, e.g., Lakso et al.

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(1992) *Proc. Natl. Acad. Sci. USA* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman et al. (1991) *Science* 251:1351-1355. If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut et al. (1997) *Nature* 385:810-813 and PCT Publication Nos. WO 97/07668 and WO 97/07669. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell, e.g., the somatic cell, is isolated.

IV. Pharmaceutical Compositions

The TANGO-69 nucleic acid molecules, TANGO-69 proteins, and anti-TANGO-69 antibodies (also referred to herein as "active compounds") of the invention can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the

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language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, 5 compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is 10 contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration 15 include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the 20 following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or 25 sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such 30 as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water 35 soluble) or dispersions and sterile powders for the

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extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof.

The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (e.g., a TANGO-69 protein or anti-TANGO-69 antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium

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and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and
5 freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin
10 capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a
15 mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and
20 the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a
25 lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring. For administration by inhalation, the
30 compounds are delivered in the form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal
35 or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to

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be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal
5 administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

10 The compounds can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared
15 with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene
20 vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova
25 Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in
30 the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit
35 form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated;

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each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

10 In therapeutic applications, anti-TANGO-69 antibodies, like other therapeutic antibodies, are administered parenterally, preferably intravenously or intramuscularly daily, monthly, biweekly, weekly, or more frequently. The preferred dosage is 0.1mg/kg to 100 mg/kg of body weight, preferably 10 to 20 mg/kg of body weight. Dosages of 50 mg/kg or higher are preferred if the antibody is to be effective within the brain. The preferred dosage for treatment of a particular disorder can be based on results observed with other therapeutic antibodies or it can be determined by one skilled based on testing in animal models. The suitable dosage of antibody in a given situation depends on the disease being treated, the severity of the disease, whether the antibody is being administered for therapeutic or preventative reasons, previous therapies administered, and the patient's clinical history. Treatment is generally continued until the desired therapeutic or preventative effect is observed. Dosage regimes of the type that can be adapted to the methods of the present invention are found in PCT Publication No. WO 94/04188.

Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible.

35 Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration

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(e.g., into the brain). A method for lipidation is described by Cruikshank et al. ((1997) *J. Acquired Immune Defic. Syndr. Hum. Retrovirol.*, 14:193-203).

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (U.S. Patent 5,328,470) or by stereotactic injection (see, e.g., Chen et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, e.g. retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

V. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: a) screening assays; b) detection assays (e.g., chromosomal mapping, tissue typing, forensic biology); c) predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and d) methods of treatment (e.g., therapeutic and prophylactic). A TANGO-69 protein interacts with other cellular proteins and can thus be used for (i) regulation of cellular proliferation; (ii) regulation of cellular differentiation; and possibly, (iii) regulation of cell survival. The isolated nucleic acid molecules of the

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invention can be used to express TANGO-69 protein (e.g., via a recombinant expression vector in a host cell in gene therapy applications), to detect TANGO-69 mRNA (e.g., in a biological sample) or a genetic lesion in a TANGO-69 gene, and to modulate TANGO-69 activity. In addition, the TANGO-69 proteins can be used to screen drugs or compounds which modulate the TANGO-69 activity or expression as well as to treat disorders characterized by insufficient or excessive production of TANGO-69 protein or production of TANGO-69 protein forms which have decreased or aberrant activity compared to TANGO-69 wild type protein. In addition, the anti-TANGO-69 antibodies of the invention can be used to detect and isolate TANGO-69 proteins and modulate TANGO-69 activity.

15 This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

A. Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, i.e., candidate or test compounds or agents (e.g., peptides, peptidomimetics, small molecules or other drugs) which bind to TANGO-69 proteins or have a stimulatory or inhibitory effect on, for example, TANGO-69 expression or TANGO-69 activity.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of a TANGO-69 protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring

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deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other
5 four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in:

- 10 DeWitt et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:6909; Erb et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann et al. (1994). *J. Med. Chem.* 37:2678; Cho et al. (1993) *Science* 261:1303; Carrell et al. (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell et al. (1994) *Angew.*
15 *Chem. Int. Ed. Engl.* 33:2061; and Gallop et al. (1994) *J. Med. Chem.* 37:1233.

- Libraries of compounds may be presented in solution (e.g., Houghten (1992) *Bio/Techniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), chips (Fodor (1993)
20 *Nature* 364:555-556), bacteria (U.S. Patent No. 5,223,409), spores (Patent Nos. 5,571,698; 5,403,484; and 5,223,409), plasmids (Cull et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:1865-1869) or phage (Scott and Smith (1990) *Science* 249:386-390; Devlin (1990) *Science*
25 249:404-406; Cwirla et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:6378-6382; and Felici (1991) *J. Mol. Biol.* 222:301-310).

- In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of
30 TANGO-69 protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a TANGO-69 protein determined. The cell, for example, can be a yeast cell or a cell of mammalian origin.
35 Determining the ability of the test compound to bind to the TANGO-69 protein can be accomplished, for example, by

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coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the TANGO-69 protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In a preferred embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of TANGO-69 protein, or a biologically active portion thereof, on the cell surface with a known compound which binds TANGO-69 to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a TANGO-69 protein, wherein determining the ability of the test compound to interact with a TANGO-69 protein comprises determining the ability of the test compound to preferentially bind to TANGO-69 or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of TANGO-69 protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (e.g., stimulate or inhibit) the activity of the TANGO-69 protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of TANGO-69 or a biologically active portion thereof can be accomplished, for example, by determining the ability of the TANGO-69 protein to bind to or

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interact with a TANGO-69 target molecule. As used herein, a "target molecule" is a molecule with which a TANGO-69 protein binds or interacts in nature, for example, a molecule on the surface of a cell which
5 expresses a TANGO-69 protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. A TANGO-69 target molecule can be a non-TANGO-69 molecule or a TANGO-69
10 protein or polypeptide of the present invention. In one embodiment, a TANGO-69 target molecule is a component of a signal transduction pathway which facilitates transduction of an extracellular signal (e.g., a signal generated by binding of a compound to a membrane-bound
15 TANGO-69 molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein which has catalytic activity or a protein which facilitates the association of downstream signaling molecules with TANGO-69.

20 Determining the ability of the TANGO-69 protein to bind to or interact with a TANGO-69 target molecule can be accomplished by one of the methods described above for determining direct binding. In a preferred embodiment, determining the ability of the TANGO-69 protein to bind
25 to or interact with a TANGO-69 target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (e.g.,
30 intracellular Ca^{2+} , diacylglycerol, IP₃, etc.), detecting catalytic/enzymatic activity of the target on an appropriate substrate, detecting the induction of a reporter gene (e.g., a TANGO-69-responsive regulatory element operably linked to a nucleic acid encoding a
35 detectable marker, e.g. luciferase), or detecting a

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cellular response, for example, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a
5 TANGO-69 protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to the TANGO-69 protein or biologically active portion thereof. Binding of the test compound to the TANGO-69 protein can be determined either
10 directly or indirectly as described above. In a preferred embodiment, the assay includes contacting the TANGO-69 protein or biologically active portion thereof with a known compound which binds TANGO-69 to form an assay mixture, contacting the assay mixture with a test
15 compound, and determining the ability of the test compound to interact with a TANGO-69 protein, wherein determining the ability of the test compound to interact with a TANGO-69 protein comprises determining the ability of the test compound to preferentially bind to TANGO-69
20 or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting TANGO-69 protein or biologically active portion thereof with a test compound and
25 determining the ability of the test compound to modulate (e.g., stimulate or inhibit) the activity of the TANGO-69 protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of TANGO-69 can be accomplished, for
30 example, by determining the ability of the TANGO-69 protein to bind to a TANGO-69 target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of
35 TANGO-69 can be accomplished by determining the ability of the TANGO-69 protein to further modulate a TANGO-69

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target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay
5 comprises contacting the TANGO-69 protein or biologically active portion thereof with a known compound which binds TANGO-69 to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a TANGO-69 protein,
10 wherein determining the ability of the test compound to interact with a TANGO-69 protein comprises determining the ability of the TANGO-69 protein to preferentially bind to or modulate the activity of a TANGO-69 target molecule.

15 The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of TANGO-69. In the case of cell-free assays comprising the membrane-bound form of TANGO-69, it may be desirable to utilize a solubilizing agent such that the
20 membrane-bound form of TANGO-69 is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton X-
25 100, Triton X-114, Thesit, Isotridecypoly(ethylene glycol ether)n, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane sulfonate (CHAPS), 3-[(3-
cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-dodecyl=N,N-dimethyl-3-ammonio-
30 1-propane sulfonate.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either TANGO-69 or its target molecule to facilitate separation of complexed from uncomplexed forms
35 of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to

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TANGO-69, or interaction of TANGO-69 with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels
5 include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase/ TANGO-69 fusion
10 proteins or glutathione-S-transferase/target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical; St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the test compound or the test compound and either
15 the non-adsorbed target protein or TANGO-69 protein, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtitre plate wells are washed to remove any unbound
20 components and complex formation is measured either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of TANGO-69 binding or activity determined using standard techniques.

25 Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either TANGO-69 or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated TANGO-69 or target
30 molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals; Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively,
35 antibodies reactive with TANGO-69 or target molecules but which do not interfere with binding of the TANGO-69

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protein to its target molecule can be derivatized to the wells of the plate, and unbound target or TANGO-69 trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those
5 described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the TANGO-69 or target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the TANGO-69 or target molecule.

10 In another embodiment, modulators of TANGO-69 expression are identified in a method in which a cell is contacted with a candidate compound and the expression of TANGO-69 mRNA or protein in the cell is determined. The level of expression of TANGO-69 mRNA or protein in the
15 presence of the candidate compound is compared to the level of expression of TANGO-69 mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of TANGO-69 expression based on this comparison. For example,
20 when expression of TANGO-69 mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of TANGO-69 mRNA or protein expression. Alternatively, when expression of
25 TANGO-69 mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of TANGO-69 mRNA or protein expression. The level of TANGO-69 mRNA or protein
30 expression in the cells can be determined by methods described herein for detecting TANGO-69 mRNA or protein.

In yet another aspect of the invention, the TANGO-69 proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, e.g., U.S. Patent No.
35 5,283,317; Zervos et al. (1993) *Cell* 72:223-232; Madura

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et al. (1993) *J. Biol. Chem.* 268:12046-12054; Bartel et al. (1993) *Bio/Techniques* 14:920-924; Iwabuchi et al. (1993) *Oncogene* 8:1693-1696; and PCT Publication No. WO 94/10300), to identify other proteins, which bind to or
5 interact with TANGO-69 ("TANGO-69-binding proteins" or "TANGO-69-bp") and modulate TANGO-69 activity. Such TANGO-69-binding proteins are also likely to be involved in the propagation of signals by the TANGO-69 proteins as, for example, upstream or downstream elements of the
10 TANGO-69 pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct,
15 the gene that codes for TANGO-69 is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to
20 a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an TANGO-69-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into
25 close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the
30 functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with TANGO-69.

This invention further pertains to novel agents identified by the above-described screening assays and
35 uses thereof for treatments as described herein.

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B. Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to:

- (i) map their respective genes on a chromosome and, thus, locate gene regions associated with genetic disease;
- (ii) identify an individual from a minute biological sample (tissue typing); and
- (iii) aid in forensic identification of a biological sample.

These applications are described in the subsections below.

1. Chromosome Mapping

Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. Accordingly, TANGO-69 nucleic acid molecules described herein or fragments thereof, can be used to map the location of TANGO-69 genes on a chromosome. The mapping of the TANGO-69 sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, TANGO-69 genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the TANGO-69 sequences. Computer analysis of TANGO-69 sequences can be used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the TANGO-69 sequences will yield an amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (e.g., human and mouse cells). As hybrids of human and mouse cells grow and divide, they gradually lose human chromosomes in random

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order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow (because they lack a particular enzyme), but in which human cells can, the one human chromosome that contains the gene encoding the
5 needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of
10 individual genes to specific human chromosomes. (D'Eustachio et al. (1983) *Science* 220:919-924). Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

15 PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using the TANGO-69 sequences to design oligonucleotide primers,
20 sublocalization can be achieved with panels of fragments from specific chromosomes. Other mapping strategies which can similarly be used to map a TANGO-69 sequence to its chromosome include *in situ* hybridization (described in Fan et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:6223-
25 27), pre-screening with labeled flow-sorted chromosomes, and pre-selection by hybridization to chromosome specific cDNA libraries.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be
30 used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical, e.g., colcemid, that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then
35 stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can

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be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases will suffice to get good results at a reasonable amount of time. For a review of this technique, see Verma et al., (Human Chromosomes: A Manual of Basic Techniques (Pergamon Press, New York, 1988)).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. (Such data are found, for example, in V. McKusick, Mendelian Inheritance in Man, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, e.g., Egeland et al. (1987) Nature 325:783-787.

Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the TANGO-69 gene can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the

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particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

10 2. Tissue Typing

 The TANGO-69 sequences of the present invention can also be used to identify individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The sequences of the present invention are useful as additional DNA markers for RFLP (described in U.S. Patent 5,272,057).

25 Furthermore, the sequences of the present invention can be used to provide an alternative technique which determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the TANGO-69 sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

 Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have

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a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The TANGO-69 sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:1 can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers which each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NO:3 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

If a panel of reagents from TANGO-69 sequences described herein is used to generate a unique identification database for an individual, those same reagents can later be used to identify tissue from that individual. Using the unique identification database, positive identification of the individual, living or dead, can be made from extremely small tissue samples.

3. Use of Partial TANGO-69 Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively

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identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, or semen found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, e.g., PCR primers, targeted to specific loci in the human genome, which can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (i.e. another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NO:1 are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the TANGO-69 sequences or portions thereof, e.g., fragments derived from the noncoding regions of SEQ ID NO:1 having a length of at least 20 or 30 bases.

The TANGO-69 sequences described herein can further be used to provide polynucleotide reagents, e.g., labeled or labelable probes which can be used in, for example, an *in situ* hybridization technique, to identify a specific tissue, e.g., brain tissue. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such TANGO-69 probes can be used to identify tissue by species and/or by organ type.

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In a similar fashion, these reagents, e.g., TANGO-69 primers or probes can be used to screen tissue culture for contamination (i.e., screen for the presence of a mixture of different types of cells in a culture).

5 C. Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining TANGO-69 protein and/or nucleic acid expression as well as TANGO-69 activity, in the context of a biological sample (e.g., blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant TANGO-69 expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with TANGO-69 protein, nucleic acid expression or activity. For example, mutations in a TANGO-69 gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with TANGO-69 protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining TANGO-69 protein, nucleic acid expression or TANGO-69 activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (e.g., drugs) for therapeutic or prophylactic treatment

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of an individual based on the genotype of the individual (e.g., the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

5 Yet another aspect of the invention pertains to monitoring the influence of agents (e.g., drugs or other compounds) on the expression or activity of TANGO-69 in clinical trials.

These and other agents are described in further
10 detail in the following sections.

1. Diagnostic Assays

An exemplary method for detecting the presence or absence of TANGO-69 in a biological sample involves obtaining a biological sample from a test subject and
15 contacting the biological sample with a compound or an agent capable of detecting TANGO-69 protein or nucleic acid (e.g., mRNA, genomic DNA) that encodes TANGO-69 protein such that the presence of TANGO-69 is detected in the biological sample. A preferred agent for detecting
20 TANGO-69 mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to TANGO-69 mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length TANGO-69 nucleic acid, such as the nucleic acid of SEQ ID NO: 1 or 3, or a portion thereof, such as an
25 oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to TANGO-69 mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

30 A preferred agent for detecting TANGO-69 protein is an antibody capable of binding to TANGO-69 protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof
35 (e.g., Fab or F(ab')₂) can be used. The term "labeled",

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with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect TANGO-69 mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of TANGO-69 mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of TANGO-69 protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of TANGO-69 genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of TANGO-69 protein include introducing into a subject a labeled anti-TANGO-69 antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

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In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting TANGO-69 protein, mRNA, or genomic DNA, such that the presence of TANGO-69 protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of TANGO-69 protein, mRNA or genomic DNA in the control sample with the presence of TANGO-69 protein, mRNA or genomic DNA in the test sample.

10 The invention also encompasses kits for detecting the presence of TANGO-69 in a biological sample (a test sample). Such kits can be used to determine if a subject is suffering from or is at increased risk of developing a disorder associated with aberrant expression of TANGO-69
15 (e.g., an immunological disorder). For example, the kit can comprise a labeled compound or agent capable of detecting TANGO-69 protein or mRNA in a biological sample and means for determining the amount of TANGO-69 in the sample (e.g., an anti-TANGO-69 antibody or an
20 oligonucleotide probe which binds to DNA encoding TANGO-69, e.g., SEQ ID NO:1 or SEQ ID NO:3). Kits may also include instruction for observing that the tested subject is suffering from or is at risk of developing a disorder associated with aberrant expression of TANGO-69 if the
25 amount of TANGO-69 protein or mRNA is above or below a normal level.

For antibody-based kits, the kit may comprise, for example: (1) a first antibody (e.g., attached to a solid support) which binds to TANGO-69 protein; and,
30 optionally, (2) a second, different antibody which binds to TANGO-69 protein or the first antibody and is conjugated to a detectable agent.

For oligonucleotide-based kits, the kit may comprise, for example: (1) an oligonucleotide, e.g., a
35 detectably labelled oligonucleotide, which hybridizes to

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a TANGO-69 nucleic acid sequence or (2) a pair of primers useful for amplifying a TANGO-69 nucleic acid molecule;

The kit may also comprise, e.g., a buffering agent, a preservative, or a protein stabilizing agent. The kit
5 may also comprise components necessary for detecting the detectable agent (e.g., an enzyme or a substrate). The kit may also contain a control sample or a series of control samples which can be assayed and compared to the test sample contained. Each component of the kit is
10 usually enclosed within an individual container and all of the various containers are within a single package along with instructions for observing whether the tested subject is suffering from or is at risk of developing a disorder associated with aberrant expression of TANGO-69.

15 2. Prognostic Assays

The methods described herein can furthermore be utilized as diagnostic or prognostic assays to identify subjects having or at risk of developing a disease or disorder associated with aberrant TANGO-69 expression or
20 activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with TANGO-69 protein, nucleic acid expression or activity, e.g.,
25 allergic diseases. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing such a disease or disorder. Thus, the present invention provides a method in which a test sample is obtained from a subject and TANGO-69 protein or
30 nucleic acid (e.g., mRNA, genomic DNA) is detected, wherein the presence of TANGO-69 protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant TANGO-69 expression or activity. As used herein, a "test
35 sample" refers to a biological sample obtained from a

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subject of interest. For example, a test sample can be a biological fluid (e.g., serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant TANGO-69 expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with a specific agent or class of agents (e.g., agents of a type which decrease TANGO-69 activity). Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant TANGO-69 expression or activity in which a test sample is obtained and TANGO-69 protein or nucleic acid is detected (e.g., wherein the presence of TANGO-69 protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant TANGO-69 expression or activity).

The methods of the invention can also be used to detect genetic lesions or mutations in a TANGO-69 gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation, or differentiation, or allergic diseases. In preferred embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion or mutation characterized by at least one of an alteration affecting the integrity of a gene encoding a TANGO-69-protein, or the mis-expression of the TANGO-69 gene. For example, such genetic lesions or mutations can be detected by ascertaining the existence of at least one of: 1) a deletion of one or more nucleotides from a TANGO-69 gene; 2) an addition of one or more nucleotides to a TANGO-69 gene; 3) a

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substitution of one or more nucleotides of a TANGO-69 gene; 4) a chromosomal rearrangement of a TANGO-69 gene; 5) an alteration in the level of a messenger RNA transcript of a TANGO-69 gene; 6) an aberrant
5 modification of a TANGO-69 gene, such as of the methylation pattern of the genomic DNA; 7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a TANGO-69 gene; 8) a non-wild type level of a TANGO-69-protein; 9) an allelic loss of a TANGO-69
10 gene; and 10) an inappropriate post-translational modification of a TANGO-69-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a TANGO-69 gene. A preferred biological sample is a peripheral
15 blood leukocyte sample isolated by conventional means from a subject.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, e.g., U.S. Patent Nos. 4,683,195 and
20 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, e.g., Landegran et al. (1988) *Science* 241:1077-1080; and Nakazawa et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:360-364), the latter of which can be particularly useful for
25 detecting point mutations in the TANGO-69-gene (see, e.g., Abravaya et al. (1995) *Nucleic Acids Res.* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the
30 sample, contacting the nucleic acid sample with one or more primers which specifically hybridize to a TANGO-69 gene under conditions such that hybridization and amplification of the TANGO-69-gene (if present) occurs, and detecting the presence or absence of an amplification
35 product, or detecting the size of the amplification product and comparing the length to a control sample. It

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is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

5 Alternative amplification methods include: self sustained sequence replication (Guatelli et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh, et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi
10 et al. (1988) *Bio/Technology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of
15 nucleic acid molecules if such molecules are present in very low numbers.

 In an alternative embodiment, mutations in a TANGO-69 gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For
20 example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA
25 indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, e.g., U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

30 In other embodiments, genetic mutations in TANGO-69 can be identified by hybridizing a sample and control nucleic acids, e.g., DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin et al. (1996) *Human Mutation* 7:244-255;
35 Kozal et al. (1996) *Nature Medicine* 2:753-759). For example, genetic mutations in TANGO-69 can be identified

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in two-dimensional arrays containing light-generated DNA probes as described in Cronin et al., *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to
5 identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by
10 using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

15 In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the TANGO-69 gene and detect mutations by comparing the sequence of the sample TANGO-69 with the corresponding wild-type (control) sequence. Examples of
20 sequencing reactions include those based on techniques developed by Maxim and Gilbert ((1977) *Proc. Natl. Acad. Sci. USA* 74:560) or Sanger ((1977) *Proc. Natl. Acad. Sci. USA* 74:5463). It is also contemplated that any of a variety of automated sequencing procedures can be
25 utilized when performing the diagnostic assays ((1995) *Bio/Techniques* 19:448), including sequencing by mass spectrometry (see, e.g., PCT Publication No. WO 94/16101; Cohen et al. (1996) *Adv. Chromatogr.* 36:127-162; and Griffin et al. (1993) *Appl. Biochem. Biotechnol.* 38:147-
30 159).

Other methods for detecting mutations in the TANGO-69 gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes (Myers et al. (1985) *Science*
35 230:1242). In general, the technique of "mismatch cleavage" entails providing heteroduplexes formed by

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hybridizing (labeled) RNA or DNA containing the wild-type TANGO-69 sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent which cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. RNA/DNA duplexes can be treated with RNase to digest mismatched regions, and DNA/DNA hybrids can be treated with S1 nuclease to digest mismatched regions.

10 In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing

15 polyacrylamide gels to determine the site of mutation. See, e.g., Cotton et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:4397; Saleeba et al. (1992) *Methods Enzymol.* 217:286-295. In a preferred embodiment, the control DNA or RNA can be labeled for detection.

20 In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in TANGO-69 cDNAs

25 obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu et al. (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe

30 based on a TANGO-69 sequence, e.g., a wild-type TANGO-69 sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or

35 the like. See, e.g., U.S. Patent No. 5,459,039.

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In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in TANGO-69 genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:2766; see also Cotton (1993) *Mutat. Res.* 285:125-144; Hayashi (1992) *Genet. Anal. Tech. Appl.* 9:73-79). Single-stranded DNA fragments of sample and control TANGO-69 nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, and the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In a preferred embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen et al. (1991) *Trends Genet.* 7:5).

In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers et al. (1985) *Nature* 313:495). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner (1987) *Biophys. Chem.* 265:12753).

Examples of other techniques for detecting point mutations include, but are not limited to, selective

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oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions which permit hybridization only if a perfect match is found (Saiki et al. (1986) *Nature* 324:163); Saiki et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:6230). Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology which depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs et al. (1989) *Nucleic Acids Res.* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition, it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini et al. (1992) *Mol. Cell Probes* 6:1). It is anticipated that in certain embodiments amplification may also be performed using Taq ligase for amplification (Barany (1991) *Proc. Natl. Acad. Sci. USA* 88:189). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits

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comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, e.g., in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or
5 illness involving a TANGO-69 gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which TANGO-69 is expressed may be utilized in the prognostic assays described herein.

10

3. Pharmacogenomics

Agents, or modulators which have a stimulatory or inhibitory effect on TANGO-69 activity (e.g., TANGO-69 gene expression) as identified by a screening assay
15 described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (e.g., inflammation, allergic diseases, HSV infections, cancer, vascular infarctions and cell death) associated with aberrant TANGO-69 activity. In conjunction with
20 such treatment, the pharmacogenomics (i.e., the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or
25 therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (e.g., drugs) for prophylactic or therapeutic treatments based on a
30 consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of TANGO-69 protein, expression of TANGO-69 nucleic acid, or mutation content of TANGO-69
35 genes in an individual can be determined to thereby

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select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, e.g., Linder (1997) *Clin. Chem.* 43(2):254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body are referred to as "altered drug action." Genetic conditions transmitted as single factors altering the way the body acts on drugs are referred to as "altered drug metabolism". These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase deficiency (G6PD) is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (e.g., N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience

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exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of TANGO-69 protein, expression of TANGO-69 nucleic acid, or mutation content of TANGO-69 genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a TANGO-69 modulator, such as a modulator identified by one of the exemplary screening assays described herein.

4. Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (e.g., drugs, compounds) on the expression or activity of TANGO-69 (e.g., the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent, as determined by a screening assay as described herein, to increase TANGO-69 gene expression, protein levels or protein activity, can be monitored in clinical trials of subjects exhibiting decreased TANGO-69 gene expression,

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protein levels, or protein activity. Alternatively, the effectiveness of an agent, as determined by a screening assay, to decrease TANGO-69 gene expression, protein levels or protein activity, can be monitored in clinical trials of subjects exhibiting increased TANGO-69 gene expression, protein levels, or protein activity. In such clinical trials, TANGO-69 expression or activity and preferably, that of other genes that have been implicated in for example, a cellular proliferation disorder, can be used as a marker of the immune responsiveness of a particular cell.

For example, and not by way of limitation, genes, including TANGO-69, that are modulated in cells by treatment with an agent (e.g., compound, drug or small molecule) which modulates TANGO-69 activity (e.g., as identified in a screening assay described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of TANGO-69 and other genes implicated in the disorder. The levels of gene expression (i.e., a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of TANGO-69 or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic

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acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) 5 detecting the level of expression of a TANGO-69 protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the TANGO-69 protein, mRNA, or genomic DNA 10 in the post-administration samples; (v) comparing the level of expression or activity of the TANGO-69 protein, mRNA, or genomic DNA in the pre-administration sample with the TANGO-69 protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering 15 the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of TANGO-69 to higher levels than detected, i.e., to increase the effectiveness of the agent. 20 Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of TANGO-69 to lower levels than detected, i.e., to decrease the effectiveness of the agent.

C. Methods of Treatment

25 The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant TANGO-69 expression or activity. Such disorders include aberrant inflammation (e.g., 30 allergies, autoimmune diseases), vascular diseases (e.g., angiogenesis, vascular infarctions, and arteriosclerotic lesions), HSV infections, disorders associated with cell death, and coagulation disorders.

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1. Prophylactic Methods

In one aspect, the invention provides a method for preventing in a subject, a disease or condition associated with an aberrant TANGO-69 expression or activity, by administering to the subject an agent which modulates TANGO-69 expression or at least one TANGO-69 activity. Subjects at risk for a disease which is caused or contributed to by aberrant TANGO-69 expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the TANGO-69 aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of TANGO-69 aberrancy, for example, a TANGO-69 agonist or TANGO-69 antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

2. Therapeutic Methods

Another aspect of the invention pertains to methods of modulating TANGO-69 expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of TANGO-69 protein activity associated with the cell. An agent that modulates TANGO-69 protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a TANGO-69 protein, a peptide, a TANGO-69 peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more of the biological activities of TANGO-69 protein. Examples of such stimulatory agents include active TANGO-69 protein and a nucleic acid molecule encoding TANGO-69 that has been introduced into the cell. In another

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embodiment, the agent inhibits one or more of the biological activities of TANGO-69 protein. Examples of such inhibitory agents include antisense TANGO-69 nucleic acid molecules and anti-TANGO-69 antibodies. These
5 modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder
10 characterized by aberrant expression or activity of a TANGO-69 protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g.,
15 upregulates or downregulates) TANGO-69 expression or activity. In another embodiment, the method involves administering a TANGO-69 protein or nucleic acid molecule as therapy to compensate for reduced or aberrant TANGO-69 expression or activity.

20 Stimulation of TANGO-69 activity is desirable in situations in which TANGO-69 is abnormally downregulated and/or in which increased TANGO-69 activity is likely to have a beneficial effect. Conversely, inhibition of TANGO-69 activity is desirable in situations in which
25 TANGO-69 is abnormally upregulated and/or in which decreased TANGO-69 activity is likely to have a beneficial effect.

This invention is further illustrated by the following examples which should not be construed as
30 limiting. The contents of all references, patents and published patent applications cited throughout this application are hereby incorporated by reference.

EXAMPLES

The present invention is based, at least in part, on
35 the discovery of a mouse gene encoding a novel TNFR-

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ligand molecule (TANGO-69), that is predicted to be a type II membrane protein and which is the murine homologue of the human HVEM ligand, LIGHT (SEQ ID NO:16).

The murine TANGO-69 cDNA (SEQ ID NO:1) described herein has a 717 nucleotide open reading frame (nucleotides 116-831 of SEQ ID NO:1; SEQ ID NO:3) which encodes a 239 amino acid protein (SEQ ID NO:2). This protein also includes a predicted intracellular domain from about amino acid 1 to amino acid 95 of SEQ ID NO:2; a predicted transmembrane domain from about amino acid 96 to amino acid 112 of SEQ ID NO 2; and a predicted extracellular domain from about amino acid 113 to amino acid 239 of SEQ ID NO:2.

Example 1: Cloning of DNA Encoding a TNF-Ligand Like Molecule

Poly A+ RNA from primary murine megakaryocyte cells was used to construct a cDNA library using the Gibco BRL kit SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning (Gibco/BRL; Bethesda, MD). Prepared cDNA was ligated into the pMET vector and subject to high throughput random sequencing using automated fluorescent dideocynucleotide sequencing and dye primer chemistry (Applied Biosystems, Inc. Foster City, CA). Initially a clone was identified that showed high homology to both human and murine Fas ligand when searched against a non-redundant protein database with the BLASTX program (Altschul et al., *J. Mol. Biol.* 215:403, 1990). This 1.7 kb clone was then fully sequenced. Further analysis of the 1.7 kb clone confirmed the homology to both human Fas ligand (Swiss Prot. Accession P48023) and murine Fas ligand (Swiss Prot. Accession P41047). Initial alignment of this clone with the human Fas ligand sequence revealed 30% identity and 54% similarity at the amino acid level.

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A full length murine cDNA clone was obtained by screening the murine megakaryocyte library with the 1.7 kb clone that was originally isolated. Screening protocols were as described by Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Press, 1989). Screening resulted in the isolation of a 1.9 kb clone that is predicted to encode a protein of 239 amino acids.

10 Example 2: Distribution of TANGO-69 mRNA in mouse and human Tissues

(a) In Situ Analysis

For detection of TANGO-69 mRNA, *in situ* hybridization was performed on (a) 8 μ m sagittal sections of fresh frozen embryonic tissue on day 12.5, 13.5, 14.5, 16.5 and postnatal day 1.5 B6 mice, and (b) on 8 μ m cross sections of adult B6 mouse liver, thymus, kidney, and on bone marrow smear preparations. Sections and smears were postfixed with 4% formaldehyde in DEPC treated 1 X PBS at room temperature for 10 minutes before being rinsed twice in DEPC treated 1 X PBS and once in 0.1 M triethanolamine-HCl (pH 8.0). Following incubation in 0.25% acetic anhydride-0.1 M triethanolamine-HCl for 10 minutes, sections were rinsed in DEPC treated 2 X SSC (1 X SSC is 0.15M NaCl plus 0.015M sodium citrate). The tissue was dehydrated through a series of ethanol washes, incubated in 100% chloroform for 5 minute, rinsed in 100% ethanol for 1 minute, and then in 95% ethanol for 1 minute and allowed to air dry.

30 The hybridization was performed using a ³⁵S- radiolabeled cRNA probe corresponding to nucleotides 223 to 751 of TANGO-69. Tissues were incubated with probe (approximately 5 X 10⁷ cpm/mL) in the presence of a solution containing 600 mM NaCl, 10 mM Tris (pH 7.5), 1 mM EDTA, 0.01% sheared salmon sperm DNA, 0.01% yeast tRNA, 0.05% yeast total RNA type X 1, 1 X Denhardt's solution,

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50% formamide, 10% dextran sulfate, 100 mM dithiothreitol, 0.1% sodium dodecyl sulfate (SDS), and 0.1% sodium thiosulfate for 18 hours at 55°C.

After hybridization, slides were washed with 2 X SSC. Sections were then sequentially incubated at 37°C in TNE (a solution containing 10 mM Tris-HCl (pH 7.6), 500 mM NaCl, and 1 mM EDTA), for 10 minutes, in TNE with 108, 25µg of RNase A per mL for 30 minutes, and finally in TNE for 10 minutes. Slides were rinsed with 2 X SSC at room temperature, washed with 2 X SSC at 50°C for 1 hour, washed with 0.2 X SSC at 55°C for 1 hour, and washed with 0.2 X SSC at 60°C for 1 hour. Sections were then dehydrated rapidly through serial ethanol/0.3 M sodium acetate concentrations before being air dried and exposed to Kodak Biomax MR scientific imaging film.

Following film exposure, a multifocal signal was present in the liver of all embryo ages examined as well as the adult bone marrow smear preparations. No signal was detected in other embryonic or adult tissues. Subsequent photoemulsion dipping and development of these slides confirmed that signal in these tissues was restricted to a discrete cell population with cellular morphology consistent with megakaryocytes or myeloid cells. To define megakaryocyte expression of TANGO-69, adult mouse bone marrow smears, prepared and fixed similar to those used for *in situ* hybridization, were immunohistochemically stained with a megakaryocyte marker. Polyclonal anti-human Von Willebrand's Factor antibody (Dako Corporation, Carpinteria, CA), a megakaryocyte marker which cross reacts with mouse Von Willebrand's Factor, stained cells identical in morphology to those cells expressing TANGO-69 mRNA.

(b) Northern blot analysis

Northern blot analysis was used to examine murine TANGO-69 expression. Murine Northern blots were purchased from Clontech (Palo Alto, CA) and were hybridized

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according to the manufacturer's directions, using a murine TANGO-69 probe. This fragment encompassed the transmembrane and the extracellular domain of TANGO-69 (amino acids 25 to 239 of SEQ ID NO:2). Northern analysis
5 revealed that TANGO-69 was expressed predominantly in the spleen and lung as a ~2 kb transcript. It was also found in the heart and in skeletal muscle as ~1.4 kb transcript. TANGO-69 transcript was not detected in brain, liver, kidney or testis.

10 Human Northern blots purchased from Clontech (Palo Alto, CA) were also probed with murine TANGO-69 as described above. A TANGO-69 transcript was detected in the same tissues as in the mouse, i.e., spleen, lung, heart and skeletal muscle.

15 Example 3: Characterization of TANGO-69 Proteins

In this example, the predicted amino acid sequence of the murine TANGO-69 protein was compared to amino acid sequences of known proteins. In addition, the molecular weight of the murine TANGO-69 protein was predicted.

20 The murine TANGO-69 cDNA isolated as described above (Figure 1; SEQ ID NO:1) encodes a 239 amino acid protein (Figure 1; SEQ ID NO:2). TANGO-69 has a predicted intracellular domain which encompasses amino acids 1-95; a predicted transmembrane domain which encompasses amino
25 acids 96-112; and a predicted extracellular domain which encompasses amino acids 113-239. Murine TANGO-69 has a predicted MW of 26.3 kDa, not including post-translational modifications. A hydropathy plot of TANGO-69 is presented in Figure 5.

30 Based on nucleotide sequence and amino acid sequence analysis, TANGO-69 is predicted to be a member of the TNFR-ligand superfamily. An alignment of murine TANGO-69 (SEQ ID NO:2) with human Fas ligand (huFASL; Genbank accession number P48023; SEQ ID NO:11) revealed that
35 murine TANGO-69 has 30% sequence identity at the

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nucleotide level and 54% sequence identity at the amino acid level with the human Fas ligand (see Figure 2).

TANGO-69 is predicted to be the murine homologue of human LIGHT. LIGHT is the ligand of the membrane bound 5 hepadnavirus entry mediator (mHVEM) (Mauri et al., supra). The alignment of murine TANGO-69 (SEQ ID NO:2) with LIGHT (Genbank accession number AF036581; SEQ ID NO:16) reveals that murine TANGO-69 has 48% identity at the nucleotide level with LIGHT and 77% identity at the amino acid level 10 with LIGHT (see Figure 3). Both TANGO-69 and LIGHT have an intracellular domain, a transmembrane domain and an extracellular domain. TANGO-69 is also expected to be a ligand of the soluble Herpesvirus Entry mediator receptor, TANGO-69-receptor (U.S. serial number _____, 15 filed _____).

Example 4: Preparation of TANGO-69 Proteins

A recombinant soluble form of the murine TANGO-69 can be produced in a variety of expression systems, for example, recombinant TANGO-69 can be produced in *E. coli* 20 and in *Pichia pastoris*.

(a) TANGO-69 expression in *E. coli*

For example, mature TANGO-69 peptide can be expressed as a recombinant glutathione-S-transferase (GST) fusion protein in *E. coli* and the fusion protein can be isolated 25 and characterized. Specifically, as described above, TANGO-69 can be fused to GST and this fusion protein can be expressed in *E. coli* strain PEB199. As TANGO-69 is predicted to be 26.3 kD and GST is predicted to be 26 kD, the fusion protein is predicted to be 52.3 kD in 30 molecular weight. Expression of the GST-TANGO-69 fusion protein in PEB199 can be induced with IPTG. The recombinant fusion protein can be purified from crude bacterial lysates of the induced PEB199 strain by affinity chromatography on glutathione beads. Using polyacrylamide 35 gel electrophoretic analysis of the proteins purified from

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the bacterial lysates, the resultant fusion protein should be 52.3 kDa in size.

(b) Preparation of TANGO-69 proteins in *Pichia pastoris*

5 Using the full length clone, a fragment was amplified by PCR. The forward primer used (SEQ ID NO:21) (5' TTTTGAATTC CTGATACAAG ATCAACGATC TCAC), corresponding to nucleotides 350-373 of mouse TANGO-69 (TANGO-69) and an added EcoRI restriction site (single underline); the
10 reverse primer (SEQ ID NO:22) (5' TTTTCTCTAGA TCACTTGTCG TCGTCGTCCT TGTAGTCGAC CATGAAAGCT CCGAAATAGG), corresponding to nucleotides 804-826 of TANGO-69, an added sequence expressing the tag DYKDDDDK (double underline), and an XbaI restriction site (single underline). The PCR
15 product was subsequently digested with EcoRI and XbaI and ligated into the pPicZα A vector (Invitrogen, Carlsbad, CA) also cut with EcoRI and XbaI (Boehringer Mannheim Biochemicals, Indianapolis, IN). The resulting plasmid fused the *Pichia pastoris* α-factor signal sequence to the
20 mature form of TANGO-69 and the C-terminal tag. Yeast (*Pichia pastoris*, strain GS115) were transformed with linearized plasmid (DraI digested) by electroporation (1500 V, 25 μF, 200 Ω) and recombinants were grown on YPDS plates containing 100 μg/mL Zeocin™ (Invitrogen, Carlsbad,
25 CA). Multiple colonies were screened for protein expression and secretion by Western blot analysis with flag-specific M2 primary antibodies (Kodak/IBI, New Haven, CT) on 10 mL BMGY cultures grown O/N at 30°C, pelleted and induced in 2 mL BMMY with 0.5% methanol over 3 days. The
30 highest yielding clone was carried forward for use in preparative scale cultures in 2L shaker flasks grown O/N at 30°C in BMGY (200 mL/flask) and seeded into BMMY media at an OD₆₀₀ = 1 (in 200 mL BMMY, 0.5 % methanol, 30°C). Supernatants were collected 3 days after induction, spun
35 (9000 rpm, 30 min., 4°C) and filtered (0.2 micron).

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Supernatants were recirculated over an M2 anti-flag antibody agarose column (Kodak/IBI, New Haven, CT) (1.6 cm diameter, 5 mL bed volume) at 2 mL/minute, 4°C for 16 hours equilibrated in phosphate buffered saline (PBS), pH 7.4, and washed in 10 column volumes of the same equilibration buffer. When eluate absorbance returned to baseline, bound protein was eluted with a 0.2M glycine, pH 3.0, step and 1.0 mL fractions collected. Peak (280nm) fractions were neutralized with 50 µl 3M Tris-HCl, pH 8.5.

10 Fractions were evaluated by SDS-PAGE (silver and/or Coomassie R-250 stained) and by Western analysis. Fractions containing significant immunoreactivity were pooled and dialysed against PBS. After high speed centrifugation (35,000 rpm, approximately 130,000 X g) for 15 1 hour at 4°C, and 0.2 µm sterile filtration, a sample was reserved and the remainder was aliquoted and frozen at -80°C. The reserved sample was then analysed by silver stained SDS-PAGE for protein purity, by Bradford assay to determine protein concentration, and by both N-terminal 20 Edman sequencing and mass spectroscopy to confirm its identity.

Example 5: Mapping of Murine TANGO-69

Murine TANGO-69 was mapped to chromosome 17 between the 2 markers D17MIT9 and D17MIT39, utilizing the Mus 25 spretus/C57BL/6J backcross panel. Forward (F) and reverse (R) primers were designed from the 3'UTR of TANGO-69 as follows;

5'-CAGGAATGGTTGGTCAGAAG (F); SEQ ID NO:23 and 5'-
CCTGTCTCCATTCCCTATTG (R); SEQ ID NO:24.

30 Amplification conditions were 35 cycles of 95°C for 1 min., 57°C for 1 min., and 72°C for 45 sec. Amplification products were separated on a 10% SSCP gel. Gels were stained with SYBR Green I and then scanned using a MD fluorimager.

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Example 6: Binding of TANGO-69-Fc to Mast Cells in the Skin

Purified TANGO-69-Fc fusion protein was used to screen tissue sections for TANGO-69-binding sites. Fresh frozen sections (8 μ m) of whole mice (postnatal day 1.5) and of skin from adult mice were prepared, fixed in acetone for 10 minutes and washed in phosphate buffered saline (PBS) for 5 minutes. Sections were then incubated in 0.3% H_2O_2 in PBS for 30 minutes to block endogenous peroxidase and washed in PBS for 5 min. After a 15 minute blocking step in PBS containing 5% goat serum, the sections were incubated with TANGO-69-Fc (10 μ g/mL in PBS/1% goat serum) for 1 hour at room temperature and then washed two times in PBS. Bound Fc fusion proteins were detected by incubating the sections with biotinylated anti-human IgG1 antibodies (10 μ g/mL, Jackson Laboratories, Bar Harbor, ME) for 30 minutes. After two washes in PBS, sections were incubated for 30 minutes with avidin-biotin-peroxidase reagent (ABC kit; Vector Laboratories, Burlingame, CA). Peroxidase activity was visualized with a diaminobenzidine tetrahydrochloride (DAB) substrate kit (Vector Laboratories, Burlingame, CA). Sections were counterstained with toluidine blue.

TANGO-69-Fc was shown to bind to a population of large granular cells in the skin of adult mice and of mice at the postnatal stage day 1.5. These cells were identified as mast cells by a toluidine blue counterstain. Human IgG1 and three control Fc fusion proteins showed no binding to mast cells. These results show that mast cells bear binding sites for TANGO-69-Fc.

Example 7: Functional role of TANGO-69

Murine TANGO-69 is expressed almost exclusively on cells of the megakaryocyte lineage. Given its very specific expression pattern, studies were done to see if TANGO-69 may also be important in platelet/endothelium interactions.

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To assess if TANGO-69 was capable of activating endothelia, human umbilical cord vein endothelial cells (HUVEC's) (Clonetics; San Diego, CA) were cultured to confluence in 6 well dishes. Purified recombinant soluble mouse TANGO-69 (amino acid 81 to amino acid 239; SEQ ID NO:7) was added to the HUVEC cultures at a concentration of 100ng/ml for 4h at 37°C. After 4h the conditioned media was collected and assayed for interleukin-8 expression by ELISA (R&D, Minneapolis, MN). Expression of VCAM-1 and E-selectin on the surface of the HUVECS was monitored by FACS using the antibodies 51-10C9 and 68-5H11 (Pharmingen, San Diego, CA). VCAM-1 and E-Selectin have been shown to be upregulated on activated or cytokine-stimulated endothelium. Fluorescence activated cell sorting (Facs) analysis of control and TANGO-69 treated cultures shows that both E-selectin and VCAM-1 are upregulated by TANGO-69. In addition TANGO-69 appears to induce synthesis of IL-8 in these cultures. In control cultures the levels of IL-8 were approximately 400 pg/mL whereas in TANGO-69 stimulated cultures IL-8 levels were approximately 7.5 times higher (3000 pg/mL).

These experiments show that TANGO-69 is involved in endothelium interactions. The endothelium comprises a crucial interface to local inflammatory responses, and is involved in the regulation of immunity, coagulation and homeostasis. Thus, TANGO-69 may be important in the initiation or regulation of these events in the endothelium.

Example 8: Effect of Increased TANGO-69 Expression on

IL-4 Production in Mice

A fragment of TANGO-69, corresponding to nucleotides 109-825 of SEQ ID NO:1, was amplified by PCR. The forward primer (SEQ ID NO:25) (5' AAAAAGAAT TCGCCCAT GGAGAGTGTG GTA), corresponds to an EcoRI restriction site (single underline) and nucleotides 109-123 of TANGO-69. The reverse primer (SEQ ID NO:26) (5' TCCTCTGTCG

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ACTCACTTGT CGTCGTCGTC CTTGTAATCG ACCATGAAAG CTCC), corresponds to nucleotides 811-825 of TANGO-69, an added sequence expressing the M2-specific tag DYKDDDDK (double underline), and a SalI restriction site (single underline). The resulting PCR product was subcloned into the retroviral vector MSCVneo (*Gene Therapy* 1:136-138). Transient transfection of 293Ebna cells (Invitrogen, Carlsbad, CA) with the TANGO-69 construct and with constructs containing viral regulatory elements resulted in the production of high titer retrovirus containing the TANGO-69 gene. This retrovirus was used to transfect bone marrow cells isolated from 5-fluorouracil treated mice. Infected bone marrow was then transplanted into sub-lethally irradiated recipient mice. Retrovirus containing no inserted gene was used as a control. This method results in the overexpression of TANGO-69 in the bone marrow derived progenitors that later move into the peripheral blood and spleen. Five weeks following transplantation, the spleens of the mice were taken for further analysis ex vivo. Single cell spleen suspensions were treated with 100 ng/mL anti-CD3 (Pharmingen, San Diego, CA) and the levels of IL-4 produced 48 hours later was measured by ELISA (Endogen, Boston, MA). The results of these experiments show that there is an approximately 85% increase in the amount of IL-4 produced by these cells. These data suggest that TANGO-69 is involved in the regulation of IL-4 production, which in turn drives IgE switching in mice.

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

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SEQUENCE LISTING

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 Thr Val Gln Val Ser Leu Leu Val Leu Leu Leu Gly Ala Gly Leu
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 50 ata caa gat caa cga tct cac cag gcc aac cca gca gca cat ctt aca
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 85 90 95
 55

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 5
 aca cga ctt ggc ctg gcc ttc ttg agg ggc ttg acg tat cat gat ggg
 501
 Thr Arg Leu Gly Leu Ala Phe Leu Arg Gly Leu Thr Tyr His Asp Gly
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[illegible]

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What is claimed is:

1. An isolated nucleic acid molecule selected from the group consisting of:

- a) a nucleic acid molecule comprising a nucleotide
5 sequence which is at least 55% identical to the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496, or a complement thereof;
- b) a nucleic acid molecule comprising a fragment
10 of at least 300 nucleotides of the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496, or a complement thereof;
- c) a nucleic acid molecule which encodes a
15 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496;
- d) a nucleic acid molecule which encodes a
20 fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2, or the polypeptide encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496; and
- e) a nucleic acid molecule which encodes a
25 naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496,
30 wherein the nucleic acid molecule hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3 or a complement thereof under stringent conditions.

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2. The isolated nucleic acid molecule of claim 1, which is selected from the group consisting of:

a) a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, the cDNA insert of
5 the plasmid deposited with ATCC as Accession Number 98496, or a complement thereof; and

b) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an amino acid sequence encoded by the cDNA
10 insert of the plasmid deposited with ATCC as Accession Number 98496.

3. The nucleic acid molecule of claim 1 further comprising vector nucleic acid sequences.

4. The nucleic acid molecule of claim 1 further
15 comprising nucleic acid sequences encoding a heterologous polypeptide.

5. A host cell which contains the nucleic acid molecule of claim 1.

6. The host cell of claim 5 which is a mammalian
20 host cell.

7. A non-human mammalian host cell containing the nucleic acid molecule of claim 1.

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8. An isolated polypeptide selected from the group consisting of:

- a) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the fragment
5 comprises at least 15 contiguous amino acids of SEQ ID NO:2;
- b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2 or an amino acid sequence encoded by the cDNA insert
10 of the plasmid deposited with ATCC as Accession Number 98496, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3 or a complement thereof under stringent conditions; and
- 15 c) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 55% identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3 or a complement thereof.

20 9. The isolated polypeptide of claim 8 comprising the amino acid sequence of SEQ ID NO:2 or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496.

10. The polypeptide of claim 8 further comprising
25 heterologous amino acid sequences.

11. An antibody which selectively binds to a polypeptide of claim 8.

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12. A method for producing a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2 or an amino acid sequence encoded
5 by the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496;

b) a polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2 or an amino acid sequence encoded by the cDNA insert of the plasmid
10 deposited with ATCC as Accession Number 98496, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2 or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496; and

15 c) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2 or an amino acid sequence encoded by the cDNA insert of the plasmid deposited with ATCC as Accession Number 98496, wherein the polypeptide is encoded by a nucleic
20 acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3 or a complement thereof under stringent conditions;

comprising culturing the host cell of claim 5 under conditions in which the nucleic acid molecule is
25 expressed.

13. A method for detecting the presence of a polypeptide of claim 8 in a sample, comprising:

a) contacting the sample with a compound which selectively binds to a polypeptide of claim 8; and
30 b) determining whether the compound binds to the polypeptide in the sample.

14. The method of claim 13, wherein the compound which binds to the polypeptide is an antibody.

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15. A kit comprising a compound which selectively binds to a polypeptide of claim 8 and instructions for use.

16. A method for detecting the presence of a
5 nucleic acid molecule of claim 1 in a sample, comprising the steps of:

- a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes to the nucleic acid molecule; and
- 10 b) determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample.

17. The method of claim 16, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

15 18. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1 and instructions for use.

19. A method for identifying a compound which binds to a polypeptide of claim 8 comprising the steps of:
20 a) contacting a polypeptide, or a cell expressing a polypeptide of claim 8 with a test compound; and
b) determining whether the polypeptide binds to the test compound.

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20. The method of claim 19, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

- a) detection of binding by direct detecting of
5 test compound/polypeptide binding;
- b) detection of binding using a competition binding assay;
- c) detection of binding using an assay for TANGO-
69-mediated signal transduction.

10 21. A method for modulating the activity of a polypeptide of claim 8 comprising contacting a polypeptide or a cell expressing a polypeptide of claim 8 with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the
15 polypeptide.

22. A method for identifying a compound which modulates the activity of a polypeptide of claim 8, comprising:

- a) contacting a polypeptide of claim 8 with a test
20 compound; and
- b) determining the effect of the test compound on the activity of the polypeptide to thereby identify a compound which modulates the activity of the polypeptide.

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M E S V V Q P S V F V 11
CTTTCCTGGGCTTCGGAGCCTCAGCTGCTCTGGC ATG GAG AGT GTG GTA CAG CCT TCA GTG TTT GTG 147

V D G Q T D I P F R R L E Q N H R R R R 31
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C G T V Q V S L A L V L L L G A G L A T 51
TGT GGC ACT GTC CAG GTC AGC CTG GCC CTG GTG CTG CTG CTA GGT GCT GGG CTG GCC ACT 267

Q G W F L L R L H Q R L G D I V A H L P 71
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D G G K G S W E K L I Q D Q R S H Q A N 91
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P A A H L T G A N A S L I G I G G P L L 111
CCA GCA GCA CAT CTT ACA GGA GCC AAC GCC AGC TTG ATA GGT ATT GGT GGA CTT CTG TTA 447

W E T R L G L A F L R G L T Y H D G A L 131
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GTG ACC ATG GAG CCC GGT TAC TAC TAT GTG TAC TCC AAA GTG CAG CTG AGC GGC GTG GGC 567

C P Q G L A N G L P I T H G L Y K R T S 171
TGC CCC CAG GGG CTG GCC AAT GGC CTC CCC ATC ACC CAT GGA CTA TAC AAG CGC ACA TCC 627

R Y P K E L E L L V S R R S P C G R A N 191
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S Y F G A F M V * 240
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FIG. 1 (1 of 2)

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TAAAAATATTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1894

FIG. 1 (2 of 2)

	1				50
huFasL	MQQPFNYYP	QIYWVDSSAS	SPWAPP GTVL	PCPTSVPRRP	GQRRPPPPPP
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muFLLM
huLTS
huTNFa
huAPO-2LM	AMMEVQGGPS	LGQTCV/LIVI
	51				100
huFasL	P.PPLPPPPP	PPPL.....P	PLPLPPLKKR	GNHSTGLCLL	VMFFMVLVAL
muFasL	PVSPLPSPSQ	PLPL.....P	..PLTPLKKK	.DHNTNLWLP	VVFFMVLVAL
muFLLMMESVQ	PSVFVVDGQT	DIPFRLEQN	HRRRCGTVO	VSLALVLLG
huLTSMGALGLE	GRGGRLOG.R	GSLLLAVAGA	TSLVTLLAV
huTNFa	..MSTESMIR	DVELAEEALP	KKTGGPQGSR	RCLFLSL...	..FSFLIVAG
huAPO-2L	FTVLLQSLCV	AVTYVYFTNE	LKQM QDKYSK	SGIACFLKED	DSYWDPNDEE
	101				150
huFasL	VGLGLGMFOL	FHLQKELAE	RESTSOMHTA	SSLEKQIGHP	SPPPEKKELR
muFasL	VGMGLGMYOL	FHLQKELAE	REFTNQSLKV	SSFEEKIANP	STPSEKKEPR
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huTNFa	ATTFLCCLHF	GVIGPQREEF	PRDLISLISPL	A..QAVRSSS	RTPSDK....
huAPO-2L	SMNSPCWQVK	WQLRQLVRKM	ILRTSEETIS	TVQEKQONIS	PLVRERGPQR
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	251				300
huFasL	NSKYPQDLVM	M.....E	GKMMSY..CT	TGQMWARSSY	LGAVFNLTSA
muFasL	NSKYPEDLVL	M.....E	EKRLNY..CT	TGOIWAHSSY	LGAVFNLTSA
muFLLM	TSRYPKELEL	L.....V	SRRSPCGRAN	SSRVWDSSF	LGGVVHLEAG
huLTS	GGAYGPGTPE	LLLEGAETVT	PVLDPARRQG	YGFLWYTSVG	FGGLVQLRRG
huTNFa	AVSYQTKVNL	L....SAIKS	PCQRETPEGA	EAKPWYEPIY	LGGVFQLEKG
huAPO-2L	TS.YDPILL	M.....	KSARNSQ...	DAEYGLYSIY	QGGIFELKEN
	301				329
huFasL	DHLYVNVSEL	SLVN.FEESQ	TFFGLYKL.		
muFasL	DHLYVNISQL	SLIN.FEESK	TFFGLYKL.		
muFLLM	EEVVVRVPGN	RLVRPRDGTR	SYFGAFMV.		
huLTS	ERVYVNISHP	DMVDFA.RGK	TFFGAVMVG		
huTNFa	DRLSAEINRP	DYLDFAESGQ	VYFGIIL.		
huAPO-2L	DRIFVSVTNE	HLID.MDHEA	SFFGAFLVG		

FIG. 2

```

      10      20      30      40      50
T69  ME-SVVQPSVFVVDGQTDIPFRRLEQNHRRRRCGTVQVSLALVLLL-GAGLATCGWFLLR
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
LIGHT MEESVVRPSVFVVDGQTDIPFTRLGRSHRRQSCSVARVGLGLLLLLMGAGLAVQGWFLLC
      10      20      30      40      50      60

      60      70      80      90      100     110
mT69 LHQRLGDIVAHLFPDGGKGSWEKLIQDQRSHQANPAAHLTGANASLIGIGGPLLWETRLGL
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
LIGHT LHWRLGEMVTRLFPDGPAGSWEQLIQERRSHEVNPAAHLTGANSSTGSGGPLLWETQLGL
      70      80      90      100     110     120

      120     130     140     150     160     170
mT69 AFLRGLTYHDGALVTMEPGYYYVYSKVQLSGVGCPOGLANGLPITHGLYKRTSRYPKELE
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
LIGHT AFLRGLSYHDGALVVTKAGYYYIYSKVQLGGVGCPLGLAS--TITHGLYKRTPRYPEELE
      130     140     150     160     170

      180     190     200     210     220     230
mT69 LLVSRRSPCGRA-NSSRVWWDSSFLGGVVHLEAGEEVVVRVPGNRLVRPRDGTRSYFGAF
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
LIGHT LLVSQQSPCGRATSSSRVWWDSSFLGGVVHLEAGEEVVVRVLDRLVRLRDGTRSYFGAF
      180     190     200     210     220     230

      239
mT69  MV
      ::
LIGHT  MV
      240

```

FIG. 3

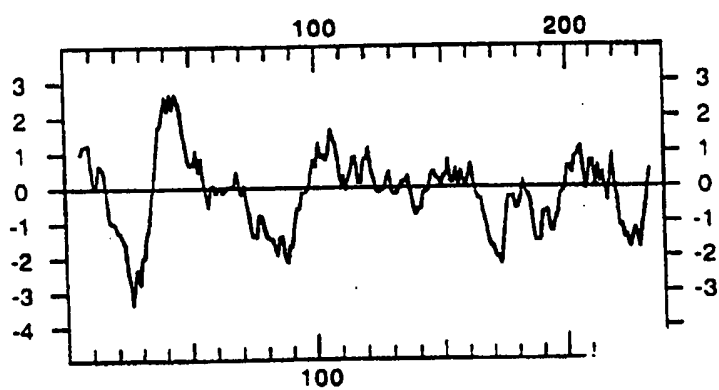


FIG. 4

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/18533

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 69.7, 325, 352, 363, 252.3, 254.11; 530/300, 351; 536/23.1, 23.4, 23.5, 24.31

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, EMBASE, CAPLUS, WPIDS
search terms: tango-69, hvem?, flm, busfield, ligand, fas ligand

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A,P	MAURI ET AL. LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are ligands for herpesvirus entry mediator. Immunity. January 1998, Vol. 8, pages 21-30, see entire document.	1-10, 12
A	NAGATA ET AL. The Fas death factor. Science. 10 March 1995, Vol. 267, pages 1449-1456, see entire document.	1-10, 12
A	YUAN, J. Transducing signals of life and death. Curr. Opin. Cell Biol. April 1997, Vol. 9, pages 247-251, see entire document.	1-10, 12



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

23 NOVEMBER 1998

Date of mailing of the international search report

24 DEC 1998

Name and mailing address of the ISA/US
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/18533

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-10,12

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/18533

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

C07K 14/435, 14/52, 14/525, C12N 5/10, 5/16, 15/10, 15/11, 15/12, 15/28, 15/63

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

435/69.1, 69.7, 325, 352, 363, 252.3, 254.11; 530/300, 351; 536/23.1, 23.4, 23.5, 24.31

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-10 and 12, drawn to nucleic acid, encoded protein, and method of using the nucleic acid to produce the protein.
Group II, claim(s) 11 and 15, drawn to antibody.
Group III, claim(s) 13 and 14, drawn to method of detecting polypeptide.
Group IV, claim(s) 15, drawn to compound, other than an antibody, which binds the polypeptide.
Group V, claim(s) 16 and 17, drawn to method of detecting nucleic acid.
Group VI, claim(s) 18, drawn to kit comprising hybridizing nucleic acid.
Group VII, claim(s) 19 and 20, drawn to method of identifying a compound which binds the polypeptide.
Group VIII, claim(s) 21, drawn to method of modulating activity of the polypeptide.
Group IX, claim(s) 22, drawn to method of identifying a compound which modulates activity of the polypeptide.

The inventions listed as Groups I-IX do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Pursuant to 37 C.F.R. § 1.475(d), this Authority considers that the main invention in the instant application comprises the first-recited product, the nucleic acid of claim 1; the first-recited method of using the product, namely the method of using the nucleic acid to produce the encoded polypeptide; and, the first-recited method of making that product, that is amplification occurring during recombinant production of the polypeptide. Further, pursuant to 37 C.F.R. § 1.475(b)-(d), the ISA/US considers that the materially and functionally dissimilar products of groups II, IV and VI and the additional methods of groups III, V and VII-IX, do not correspond to the main invention. This Authority, therefore, considers that the several inventions do not share a special technical feature within the meaning of PCT Rule 13.2 and thus do not relate to a single general inventive concept within the meaning of PCT Rule 13.1.